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US-10-909-125-801
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US-10-10-1086-75
US-11-121-086-37
US-11-121-086-37
US-11-121-086-54
US-11-121-086-78
US-10-750-185-6287
US-10-750-185-43919
US-11-191-668-3
US-11-191-668-3
US-11-191-668-71
US-10-750-185-43919
US-11-191-688-71
US-10-750-185-43422
US-11-027-964-2
US-10-750-185-6034
US-10-750-185-50341
US-10-750-185-54507
US-10-750-185-54507

Sequence 3898, Ap Sequence 801, App Sequence 815, App Sequence 75, Appl Sequence 95, Appl Sequence 54, Appl Sequence 54, Appl Sequence 63154, A Sequence 63154, A Sequence 3, Appli Sequence 3, Appli Sequence 24686, A Sequence 24686, A Sequence 43919, A Sequence 43919, A Sequence 3, Appli Sequence 43910, A Sequence 43910, A Sequence 6308, A Sequence 6308, A Sequence 6301, Appli Sequence 63407, A Sequence 6341, A

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1: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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length: 2000000000
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Listing first 45 summaries
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WS-11-117-187-203
WS-10-750-185-55754
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US-10-750-185-5414
US-10-131-826A-533
US-11-121-086-49
US-11-117-187-209
US-11-117-187-209
US-10-750-185-54249
US-10-750-185-49243
US-10-750-185-61642
US-10-750-185-61642
US-10-750-185-61642
US-10-750-185-61642
US-10-750-185-628397
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           Sequence 203, App
Sequence 55754, A
Sequence 55754, A
Sequence 531, App
Sequence 86, Appl
Sequence 199, Appl
Sequence 209, Appl
Sequence 209, Appl
Sequence 49243, A
Sequence 61642, A
Sequence 211, Appl
Sequence 211, Appl
Sequence 211, Appl
Sequence 211, Appl
Sequence 52397, A
Sequence 50, Appli
Sequence 50, Appli
Sequence 102, Appli
Sequence 40390, A
Sequence 40390, A
Sequence 40322, Appli
Sequence 40390, Appli
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503 AGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTACAATAAAGAAAATAAACCAAG 561	443 AAATGTGCATAACTTAAAAAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCCTTGGAAA 502	383 CTGAGAAAACTGATGTTGGTAACTTGATTTAATATACAACTGGGTTAAAATAAAAA 442	323 CCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTG 382	263 GTTTCCTCTGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATTAATCAGG 322	Query Match 3.7%; Score 44.6; DB 7; Length 96583; Best Local Similarity 46.8%; Pred. No. 0.17; Matches 140; Conservative 0; Mismatches 159; Indels 0; Gaps 0;	US-11-117-187-203 US-11-117-187-203 US-11-117-187-203 Sequence 203, Application US/11117187 Publication No. US20050266560A1 GENERAL INFORMATION: APPLICANT: PREUSS, DAPHNE APPLICANT: CORENHAVER, GREGORY TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS FILE REFERENCE: ARCD:309US CURRENT APPLICATION NUMBER: US/11/117,187 CURRENT APPLICATION NUMBER: US/99/531,120 PRIOR APPLICATION NUMBER: US/99/531,120 PRIOR APPLICATION NUMBER: US/99/531,120 PRIOR FILING DATE: 2000-03-17 PRIOR FILING DATE: 1999-03-18 INUMBER OF SEQ ID NOS: 212 SOFTMARE: Patentin Ver. 2.1 SEQ ID NO 203 LENGTH: 96583 TYPE: DUA ORGANISM: Arabidopsis thaliana US-11-117-187-203

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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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US-10-750-185-55754/c
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US-10-750-185-25798
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
LENGTH: 1711
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Best Local
SOFTWARE: PatentIN version 3.1
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Publication No. US20050260603A1
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
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                                                                                                                                                                                                                                                                                                                                                                                                                                      823
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Pred. No. 0.073;
0; Mismatches 161;
                                                                                                                                   BOVINE
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US-10-750-185-54114/c
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LENGTH: 1593
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                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTMARE: Patentin version 3.1
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Best Local Similarity
Matches 140; Conserv
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LENGTH: 1625
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
FILE REFERENCE: MMIII00-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MMI GENOMICS,
APPLICANT: DeNISE, Sue I
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, Da
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1514 ATAAAATAAATACTTGTAAGCAACAAAACAAAAAACCACAAAGCTTATGTATTTTATTT
                             432 AAAATAAAAAAAAATGTGCATAACTTAAAAAAAAAACCAAATACCAACAAGACTTTACTT
                                                                                     372 ACATGTGAGTGCTGAGAAAACTGATGTTGGTAACTTGATTTAATAATATCAAACTGGGTT
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                                                                                                                                        l Similarity
70; Conserv
                                                                AAAATTGATTGCATAGAATAATGATGCTGTTAACATTTTTCTATGGTCTTAGAATTTGAT
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KERR, Richard
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Pred. No. 0.32;
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Pred. No. 0.12;
0; Mismatches 164; Indels
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US-10-131-826A-533

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Matches
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                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 533
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                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/059113 PRIOR FILING DATE: 1997-09-17
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                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
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NAME/KEY: unsure
                                                                                                                                                                                                                                                                          OCATION: 396
                                                                                                                                                                                                                                                                                                                                                            ENGTH: 496
                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/059184 FILING DATE: 1997-09-17
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FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/059588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059122
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FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/059352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-09-18
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   448
                                 328 CCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAG 387
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                                                                                                                                                                                       Similarity
TGCATAACTTAAAAAAAAAACCAAATACCAACAAGA 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumas,Daniel
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                                                                                                                                                                        Conservative
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                                                                                                                                                                   Score 39.4; DB Pred. No. 0.24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            See File Wrapper or PALM
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US-11-117-187-199/c
; Sequence 199, Application US/11117187; Publication No. US20050266560A1; GENERAL INFORWATION:
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Sequence 86, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.

APPLICANT: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138.6000-00000

FILE REFERENCE: 09138.6000-00000
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; ORGANISM: Arabidopsis thaliana US-11-117-187-199
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                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 199
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                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                        APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS
FILE REFERENCE: ARCD:309US
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CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
                                                                                                                          PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                  APPLICANT: PREUSS, DAPHNE APPLICANT: COPENHAVER, G
                                        TYPE: DNA
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ORGANISM: Homo sapiens
                                                            LENGTH: 101786
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Pred. No. 6.7;
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CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
VUMBER OF SEQ ID NOS: 212
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 209
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US-11-117-187-209
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US-11-121-086-49
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Best Local :
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                                                                                                                                                                                                                                                                              APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
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APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

CURRENT FOR STATE CONTROL OF STATE CONTROL O
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91; Conservative
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Pred. No. 6.8;
0; Mismatches 87;
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 54249
LENGTH: 789
TYPE: DNA
ORGANISM: Bovine 19866881847788
US-10-750-185-54249
RESULT 11
US-10-750-185-49243
; Sequence 49243, Application US/10750185
; Publication No. US20050260603A1
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US-10-750-185-54249
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-209
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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Best Local Similarity
Matches 113; Conserv
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MMI GENOMICS, I. APPLICANT: DENISE, Sue K. APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                              Local Similarity 52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201773 AAGTTCAAATACAAAATTTATTTAATTTAAACAAAAAACGTTTAGTAAGAATAATATT 201829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646 TGCAAGCTTAGCCTACAAACGAGCAGACAGACAACAGAGCC 686
                                                                                                                                                                              269 GACCAATAGCCCAACAAATTCACCTAGATTGAATATTGAGAACAAAAAGCTTACACTGAA
                                                                                                                                                                                                                586 TCCTAAAAGAACAGAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTC
                                                                                                                                                                                                                                                  209 TAGCAAATACATTAGCAATGAAAAATATCATTGAAGAAAACCCTATAGATCTATTCTAT
                                                                                                                                                                                                                                                                                     526 TAGCCTTTATATTTACAATAAAGAAATAAACCAAGGTCCCGATATAGCTGTAATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AGTATTTTGTGTTAAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTGGTAACTTGA 409
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                                                                                                              AGGGGACATATCGTACACAAAAATAAACAGGAGAAACTGCC
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nilarity 47.7%;
Conservative
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Pred. No. 21;
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APPLICANT: APPLICANT:

ROSENFELD, David HOLM, Tom

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, II APPLICANT: DeNISE, Sue K. APPLICANT: KERR, Richard

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US-10-750-185-61642; Sequence 61642, Application US/10750185; Publication No. US20050260603A1
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; ORGANISM: Bovine
US-10-750-185-49243
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SEQ ID NO 61642
LENGTH: 3631
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 49243
                                                                              Matches 105;
                                                                                               Query Match
Best Local Similarity
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Best Local Similarity 50.8%;
Matches 90; Conservative
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISE, Sue K. APPLICANT: KERR, Richard
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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                          559 AAGGTCCCGATATAGCTGTAATTTTATTCCTAAAAGAACAGAAACTTTCACTATGCT 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655 TAGGATGTTAAGTATCTTAACTTTTTAACAGTACATATTAGAAAGTTGCTTTCTACT 711
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                                                                              Conservative
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                                                                                               3.1%;
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                                                                        Score 37.8; DB 6;
Pred. No. 2;
0; Mismatches 112;
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                                                                                                                Length 3631;
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US-11-117-187-211/c
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US-10-793-626-3381
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                                                                                                                                               Sequence 211, Application US/11117187 Publication No. US20050266560A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3381
LENGTH: 4071
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GENERAL INFORMATION
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Publication No. US20050255478A1
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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les 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1500
                                                                                                                                                                                                                                                                                                                          1620 AAAATTGATCTAGAAGTATTCATATTATCTTTAATATCTTC 1660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 TTGTTTCCTCTCGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATTAATCA 320
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45.9%; Pred. No. 2.1;
ative 0; Mismatches
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PRIOR APPLICATION NUMBER: US/09/531,120

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APPLICANT: PREUSS, DAPHNE
APPLICANT: PREUSS, DAPHNE
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR PRILING DATE: 2000-03-17
PRIOR PRILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PATCHINI DAS: 212
SOFTWARE: PATCHINI Ver. 2.1
SEQ ID NO 211
TYPE: DNA
GRGANISM: Arabidopsis thaliana
US-11-117-187-211
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; ORGANISM: Arabidopsis thaliana
US-11-117-187-211
                                                                                                                                                                                                                                                                          Query Match 3.1%; Score 37.6; DB 7; Length 1082144; Best Local Similarity 48.6%; Pred. No. 50; Matches 103; Conservative 0; Mismatches 109; Indels 0;
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PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 211
LENGTH: 1082144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 211, Application US/11117187 Publication No. US20050266560A1 GENERAL INFORMATION:
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Best Local Similarity 50.3%;
Matches 93; Conservative
                                                 556880 ATATGTAAAATAATTTTGTCCATATTTAAATCAAAAGGTGTATTTTTAGTAAAATCA 556939
                                                                                                                            556820 GATATGAAATTATATTTATTTTTACACTCGCATATTTAGGCGGGCATTACCTAGTTTTT
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594 GAACAGAAACTTTCACTATGCTTTAAAATTAA 625
                                                                             534 ATATTTACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCTAAAA 593
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Pred. No. 44
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Db 556940 AAACTAAATTAAAAAATTGAGAGAAAAAGAA 556971

Search completed: December 12, 2005, 15:45:07 Job time : 249 secs

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Database
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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1220
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 18	c 17	c 16	15	14	ü	12	c 11	10	ø	8	c 7	6	o u	4.	w	2	ъ	Result No.
57.6	58	139.4	140.6	143.4	146.92	176.2	190.6	213	236.8	237.4	238	238	239	243.4	793.4	793.4	1218.4	Score
4.7	4.8	11.4	11.5	11.8	12.0	14.4		17.5	19.4	19.5	19.5	19.5	19.6	20.0			99.9	Query Match
13925	2000	2846	2846	763	132392	290	221218	2424	2471	6714	240825	240825	183215	191377	326993	228774	228046	Query Match Length
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	AX655393 Sequence	AX458642 Sequence	AX458641 Sequence	AJ289781 Homo sapi	AC141003 Rattus no	Z57119 H.sapiens C	AC152689 Bos tauru	AF004326 Mus muscu	BC027216 Mus muscu	AY563557 Homo sapi	AX523960 Sequence	AX087869 Sequence	AC091095 Homo sapi	AC018398 Homo sapi	AC132960 Rattus no	AC114046 Rattus no	AC129567 Mus muscu	Description

REFERENCE AUTHORS

3 (bases 1 to 228046)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.

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4.2	4.2	4.2	4.2	4.2	4.2	2	'n	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.4	4.4	4.4	4.4		4.5	4.5	4.5	4.5
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AX767564	AX767488	AX344713	CQ807186	CQ806912	YSCMTCG07	AY701231	CR847902	AC128556	BX294132	AC117176	AB101024	CR388102	CR847960	BX936345	AC115592	AC156865	AB101022	AB101021	AC116957_1	AC116957_0	CR394545	PFMAL13_25	AX347043	CR855390	AX345795	AC162359
		AX344713 Sequence	CQ807186 Sequence	CQ806912 Sequence	L36891 Saccharomyc	AY701231 Orconecte	CR847902 Danio rer	AC128556 Rattus	BX294132 Zebrafish	AC117176 Dictyoste	AB101024 Carabus m	CR388102 Danio rer	CR847960 Danio rer	BX936345 Danio rer	AC115592 Dictyoste	AC156865 Bos tauru	AB101022 Carabus m	AB101021 Carabus m	Continuation (2 of	AC116957 Dictyoste	CR394545 Zebrafish	Continuation (26	AX347043 Sequence	CR855390 Danio rer	AX345795 Sequence	AC162359 Bos tauru

ALIGNMENTS

RESULT 1 AC129567

JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS TITLE VERSION KEYWORDS DEFINITION ACCESSION SOURCE COCUS JOURNAL TITLE ORGANISM CEB 2 (bases 1 to 228046)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Canarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyan, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nauyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Litter, Submission Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Mus musculus chromosome Unpublished 1 (Dases 1 to 228046)
1 (Dases 1 to 228046)
Birren, B., Nusbaum, C. and Lander, E.
Birren, B., Chromosome 8, clone RP23-50L10 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. Mus musculus chromosome AC129567 AC129567.8 GI:46240921 Direct Submission Mus musculus Mus musculus (house mouse) 228046 bp DNA linear ROD 06-APR-ne 8, clone RP23-50L10, complete sequence. ROD 06-APR-2004

FEATURES Location/Qualifiers 1. 228046 /organisms="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="8" /clone="RP23-50L10" /clone="RP23-50L10" /clone_ib="RPCI-23 Female Mouse BAC" 1. 408 /note="wgs_end_extension clone_end:SP6" /rpt_family="(TG)n"	On Apr 6, 2004 this sequence version replaced gi:42794163. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html Center: Whitchead Institute/MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@broad.mit.edu Center project Information Center project name: 50_L_10		Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Derris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagophan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Sanare, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submitsed (07-MAR-2004) Whitehead Institute/MIT Center for Genome and College of the Street, Cambridge, MA 02141, USA (1986) 1 to 228046 (1986) 1 to
	t_region complete (t_region complete) /rpt complete (t_region complete) /t_region complete (t_region complete) /rpt complete (t_region complete) /rpt complete (t_region complete)	repeat_region 49465135 repeat_region 51515503 /rpt_family="MTD" repeat_region /rpt_family="MTD" repeat_region /rpt_family="B4A" /rpt_family="B4A" /rpt_family="RMER15" repeat_region /rpt_family="RMER15" /rpt_family="RMER15" /rpt_family="RMER15" /rpt_family="RMER15" /rpt_family="RMER15" /rpt_family="B1D9" repeat_region /rpt_family="A-rich" /rpt_family="GGGTG)n" repeat_region /rpt_family="GGGTG)n" repeat_region /rpt_family="MER34" repeat_region /rpt_family="MER34" repeat_region /rpt_family="MT-int" repeat_region /rpt_family="MT-int"	

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CAGTCCTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCC
                                               CTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTGTGTTCCCAGAAGGCTTCTGCAGTACA
                                                                                                            CAAACGAGCAGACAGACAGAGCCCCAGCTACTCTCTAGGAAATAATTAGGGTGGTGC
                                                                                                                                                                    AACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGCCTA
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                             CTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTGTGTTCCCAGAAGGCTTCTGCAGTACA 166248
                                                                                                                                                                                                             CAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCTAAAAGAACAGA
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complement(15813. .16133)
/rpt family="MTE"
complement(16623. .16776)
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18154.
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17613
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15539. .15602
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15604. .15705
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Pred. No. 1.8e-270;
0; Mismatches 1;
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                                             AC114046.4 GI:30581607
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                      Rattus norvegicus
                                                                                                    AC114046 228774 bp D
Rattus norvegicus clone CH230-187J8,
                                                                                         AC114046
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                                                                                                                                                                                                                                                                                    GAGCCTGCTGCGGGACGGAGAAGGCTCTCACTGATGGACTTATTCACACGGCACAGCCCT
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                            Euteleostomi;
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REFERENCE AUTHORS

CE 1 (bases 1 to 228774)

CE 1 (bases 1 to 228774)

RS Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Clavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Desper, H., Dugan-Rocha, S., Dumn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Hanelarson, N., Henderson, N., Hernandez, J., Hernandez, J., Hardway, Y., Handk, P., Handerson, N., Hernandez, J., Hernandez, J., Handerson, N., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Li, Z., Liu, J., Lood, H., Levan, J., Lewis, L., Li, Z., Liu, J., Lovals, H., Levan, J., Lewis, L., Li, Z., Liu, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Mahiloy, K., Mangum, A., Mahindertne, M., Mahindertne, M., Mahnoud, M., Malloy, K., Mangum, A., Mander, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, A., Mahinder, M., Mah

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Milosaylsvic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Manphy, M., Mark, J., Markerris, C., Weal, D., Newton, N., Mynyen, N., Morris, S., Manphy, M., Mark, J., Markerris, C., Weal, D., Newton, N., Mynyen, N., Morris, S., Manphy, M., Mark, J., Marker, M., Morris, S., Marker, M., Morris, M., Marker, M., Mar
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TGGCTGGTCTGTGTTCCCAGAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCAC
                                                                                GCCCCAGCTACTCTAGGAAATAATTAGGGTGGTGCCTCTGACATGCCCCAGGGGTCTTG
                                                                                                                   GCCCCAGCTTCTCTCTAGGAAATAATTAGGGTGGTGCCTATGACATGCCCAGGGGTCTTG
                                                                                                                                                                                      CCTAAAAAACAAACAAACAAACAAAAAAAAACCAGAAACTTTCCCTATGCTTTAAAATT
                                                                                                                                                                                                                                                                                AGCCTTTATATTTTACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATT
                                                                                                                                                                                                                                                                                                                                          ACCAAATACCAACAAGACTTTACTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTT 526
                                                                                                                                                     ---AAAAACCAGCAGAACTTTACTTCCCTTTGGAAAAACACAATTTTAAGGGCCGATCTT
                                                                                                                                                                                                                                                                                                                                                                                         TTTAATAATATCAAACTGGGTTAAAAT---AAAAAAAATGTGCATAACTTAAAAAAAAA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTATTCTGTGTTAAAGGTAAAAAACATGTAAGTGCTGAG--AAGCTGACCTGATAACTTGA
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                                                                                                                                                                                                                                                     ACTCTTTATATTTACAATAAAGAAAATAAACCA--GTCCTAATATAGCTGTAGTTTTATT 8338;
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1 228774: contig of 228774 bp in length.
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227275. .228774
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                             ----AAAAGAACAGAAACTTTCACTATGCTTTAAAATT
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, B., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Ballen, C., Allen, H., Ballen, C., Barber, M., Barnstead, M., Benahmed, F., Balewin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Gebregorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, J., Hernandez, J., Hadun, S. L., Hodgson, A., Hornandez, J., Hadun, S. L., Hodgson, A., Hornandez, J., Jackson, L., Jackson, L., Jackson, L., Jackson, R., Johnson, C., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., London, P., Longacre, S., Liu, J., Liu, J., Lon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84036 AAGAATGTG 84044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1212 GAGAGAATG 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 TATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGGAAGATAGTGGGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus clone CH230-162J3,
***, 16 unordered pieces.
AC132960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC132960
AC132960.3 GI:25073326
HTG; HTGS_PHASE1; HTGS_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAGGAAAGTGATTGATTCGGATACTGACACTGTAGACTCAGGGGAGAAACAAAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCAGGACTCCTATGTGCCTGCAAGTTTGCTGAACTCACAGTTTAGAACCCCAAAGAGAGA 84035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGGAGAAGAAGAGAAGACAGGCACTGGGAAAGAGCCTGCTGCGGGACGGAGAAG 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGGGGCGGAGCGGCTGCCACATGTCTGGCTGCTCTTATCAACTTATCATATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGGGGCCGAGCCTGCCTGCACATGTCTGGCTGCTCTTATCAACTTATCATATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGGAAGACAGTGGGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCAGGAC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCTCACTGATGGACTTATTCACACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAGAG 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTGCAGACCTCTGGAGTGAGCAGGGCTGCTTCCTTCTCAGGACAGCTCCCTGTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGCAGACCTCTGGAGTGAGCAGGGCTGCTCCTTCCTCTCAGGACAGCTCCGAGTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGGAAAGTGATTCGGATACTGACACTGTAGGCTCAGGGGAAAACAAAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 326993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GCAAGTTTGCTGAACTCACAGTTTAGAACCCAAAAAAGAGA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA 11116a.
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IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83975
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AL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23322544.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome spatial and the contigs within a contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Milosavijevic, A., Minder,G., Minda,E., Montemayor, J., Moore,S., Milosavijevic,A., Minder,G., Munidasa,M., Murphy,M., Nair,L., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Namkervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Parks,K., Naokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pul,-L., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pul,-L., Plopper,F., Roindexter,A., Popovic,D., Primus,E., Pul,-L., Plopper,F., Roindexter,A., Reeves,K., Regter,M.A., Reigh,R., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Shetty,J., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhoo,S., Dunn,D., von,V., Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
3 (bases 1 to 35693)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahhmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 326993)
Rat Genome Sequencing Consortium.
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USA
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TITLE JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

Center project name: KCDZ

Center clone name: CH330-162J3

Center clone name: CH330-162J3

Assembly program: Phrap; version 0.990329

Consensus quality: 276174 bases at least Q30

Consensus quality: 28235 bases at least Q30

Consensus quality: 288610 bases at least Q20

Estimated insert size: 281736; sum-of-contigs estimation Quality coverage: 5x in Q20 bases; sum-of-contigs estimation Center code: BCM Center: Baylor College Genome Center of Medicine

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces

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FEATURES
Source
                                                                                                         gap
                                                                                                                                                    misc
                         gap
                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314034
315122
315623
316623
316723
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317909
317909
319429
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320860
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320960
3223511
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41183
47338
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51041
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278325
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312761
312861
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22718
36670
36770
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47438. .49026
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5479. .58
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51041. .51140
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41083. .41182
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22718. .23793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cione_end:Sp6
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                                                                                                                                                                                                                                                                            36670.
                                                                                                                                                                                                                                                                                                                                                                                                  /note="wgs_contig"
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36670. .36769
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35557. .36669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="CH230-162J3"
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22617: contig of 22617 bp in length
22717; gap of unknown length
36669: contig of 13952 bp in length
36669: contig of 13952 bp in length
41082: contig of 4313 bp in length
41082: contig of 6155 bp in length
47337: contig of 6155 bp in length
47437: gap of unknown length
51140: contig of 6165 bp in length
51140: gap of unknown length
51140: gap of unknown length
51140: contig of 227184 bp in length
51140: contig of 227184 bp in length
512760: contig of 127184 bp in length
512760: contig of 127184 bp in length
312760: gap of unknown length
313933: contig of 1073 bp in length
315121: contig of 1073 bp in length
315121: gap of unknown length
315722: gap of unknown length
315722: gap of unknown length
316622: contig of 1086 bp in length
317908: gap of unknown length
317908: gap of unknown length
319328: contig of 1401 bp in length
319328: contig of 1431 bp in length
319428: gap of unknown length
320859: gap of unknown length
322300: contig of 1341 bp in length
322400: gap of unknown length
322510: contig of 1341 bp in length
322510: contig of 110 bp in length
32290: contig of 1341 bp in length
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JOURNAL REFERENCE
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AUTHORS
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                                                                                                 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Porrest, C., Galegan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Tehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirreil, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
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Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome
                                               Zimmer, A. and Zody, M. Direct Submission
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Birren, B., Linton, L.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Homo sapiens chromosome 8, clone RP11-16G12, complete sequence
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RES 1 to 191377)

CE 4 (bases 1 to 191377)

RRS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chargen, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Charger, B., Brown, A., Campopiano, A., Chang, J., Chang, J., Chang, J., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Grand, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., McCarthy, M., McEwan, P., McKernan, K., Mardhis, J., Meneus, L., Micol, R., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Norbu, C., Nacoha, C., Nacohan, P., McKernan, K., Meldrim, J., Meneus, L., Norbu, C., Nacohan, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Roynan, C., Weil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Reil, D., O'Reil, D., O'Connor, T., O'Donnell, P., O'Neil, D., Neil, D., Nacohaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Setnaus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Voa, M., Wille, R., Wille,
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(B 3 (bases 1 to 191377)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
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Viel, R., Vo, A., Wilson, B., Wi, X., Wyman, D., Ye, W.J., Young, G.,
Direct Submission
Al., Submitted (19, ADR-2002) Whithhead Institute/MTT Contex for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 19, 2002 this sequence version replaced gi:20148178. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                             GAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGCC 658
                                                                                                                                                                                                                                                                                                AAGAAATAAACCAAGGTCCCGATATAGGTGTAATTTTATTCCTA------AAAGAACA 598
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                                           CTGCAGCATGGGTCCTGGTTGGAGGGCAGGCATTCTGCTCTGATTTTTCCTGTTGCCTGG
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                                                                                                                                                              ACAAAATAAACCGAAGTCCTGACCTATTTGTAATATTTTTATTCCTAAAGGAAAAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                         ТАЛАЛА ----- АЛАЛІ ТІССАТЛАСТТАЛАЛАЛАЛАССАЛАТАССАЛСАЛ ВАСТТІЛ 488
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                                                                                                                                  GGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCAGAAGGCTT
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28205. .28272
/rpt family="GA-rich"
28663. .28682
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9. .31699
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. .30036)
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                                                                                                                                                                                                                                                                Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                             Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 8, 2001 this sequence version replaced gi:13487963 All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, 22 unordered pieces.
AC091095
AC091095.2 GI:14626897
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-MAR-2001) Whitehead Institute/MIT Center for Genome
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                 (bases 1 to 183215)
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Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                     Web site: http://www-seg.wi.mit.edu
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me 8, clone
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NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 163000; agarose-fp Insert size: 181115; sum-of-contigs Quality coverage: 9.2 in Q20 bases; Quality coverage: 8.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 174312 bases at least Q40 Consensus quality: 178687 bases at least Q30 Consensus quality: 180102 bases at least Q20
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vector_side:left"
49246. ..49345
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1. .49245
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                                                                                                                                                             organism="Homo sapiens"
                                                                                       clone="RP11-77H21"
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_xref="taxon:9606"
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49345: gap of 100 bp
49956: contig of 611 bp in length
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                                                                                                                                                                                            'Qualifiers
                                                                                                                                                                                                             contig of 100 pp
gap of 100 pp
gap of 100 pp
contig of 61042 bp in length
qap of 100 bp
                                                                                                                                                                                                                                                                                 gap of 100 bp
contig of 10395 l
gap of 100 bp
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                                                                                                                                                                                                         contig of 61042 bp
gap of 100 bp
contig of 27530 bp
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g of 1193 bp in length
f 100 bp
g of 1111 bp in length
f 100 bp
g of 725 bp in length
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g of 1617 bp in length
f 100 bp
g of 1440 bp in length
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of 787 bp
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of 654 bp
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of 915 bp
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of 2423 bp in length
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100 bp
of 719 bp in length
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of 994 bp in length
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of 801 bp in length
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of 653 bp in length
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of 588 bp in length
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Indels

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Gaps

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/note="assembly_fragment"
49957. 50056
/estimated_length=100
50057. 50739
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60716. .60815
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58198. .58998
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58999. .59098
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65727. .68
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3350. .63449
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53362. .54015
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50740. .50839
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54116. .54768
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50840. .51558
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Sequence 1 from Patent WO0114550.
AX087869
AX087869.1 GI:13396862
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                           Homo sapiens
             Hominidae; Homo.
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exon 3737737466 /note="exon S" primer_bind 3955639574 /note="4-59.rp"	exon 3426134404 /note="exon F"	exon 31357. 31471 /note="exon E"	exon 2681026897	mplement"	not		בו ב	riation	- binding	/note="5-392-222.mis complement" primer bind 1026710285	/note="5-392-222 : polymorphic base G or T" primer_bind 1022910247	<pre>variation 10228</pre>	.mls"		exon 10115 10233	֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	<pre>primer_bind 48914908 /note="5-391.rp complement"</pre>		mer_bind	- ;	ation	<pre>misc binding 4589. 4613</pre>	primer_bind 4582. 4600	primer_bind 45594577	<pre>primer_bind 21082125 /note="5-390.rp complement"</pre>		er_bind		riation 1999	misc binding 19872011	primer_bind 19801998	primer_bind 1820. " 1840" region	misc_feature 12000 /nore="stream atory region"	/mol_type="unassigned DNA" /db xref="taxon:9606"	source		AUTHORS Barry,C., Chumakov,I. and Blumenfeld,M. TITLE Prostate cancer-related gene 3 (pg3) and biallelic markers thereof JOURNAL Patent: WO 0114550-A 1 01-MAR-2001;
/note="9" rimer_bind 69182 . /note="4 /note="4 /note="4 rimer_bind 69502	r bind	nrimer hind 67476 67494	t i or	h 1	/note="9 r bind 67456	primer_bind 6728967309	exon 50436, .50545		mis complements	variation 42232 / variation /not=="4-51-312 : nolymorphic hase G or C"	<pre>misc_binding 4222042244 /bound moiety="4-51-312.probe"</pre>	<pre>primer_bind 4221342231 /note="4-51-312.mis"</pre>	r_bind	r_bind 41564. /note="	/note="	r bind 4140s	/bound_	/note= binding 41392.	/note="4-54-199 : polymorphic base A or C" primer_bind 4138641404	variation 41385	primer_bind 4138541403	misc_binding 4137341397 /bound moiety="4-54-199.probe"	primer_bind 4136641384 /note="4-54-199.mis"	/note="	/note="	/note=" r bind 40242.	/note="4-58-289 : polymorphic base G or C" primer bind 3997439992	шотегу≈ 4-5	.39985		bind	_bind 39945. /note="		misc_pinding 3993239936 /bound_moiety="4-58-318.probe" variation 39944	er_brind 3923. /note="	/notes"	exon 3970440858 /note="exon T" primer bind 3987739896

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GGTCCCGATATAGCTGTAATTTTATTCCTA----AAAGAACAGAAACTTTCACTATG
                       GCACACGTTTACAGGAGCCAAACTTCTTCCTCTTTATTTGTAATAACAAAAATAAACCGA
                                             GCACATTTACAAGGG----CTGATCTTAGCCTTTATATTTACAATAAAGAAAATAAACCAA
                                                                                     AATGTGCATAACTTAAAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCCTTGGAAAA 503
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81241. .81265
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69521
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TITLE
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Pg-3 and biallelic markers thereof
Patent: WO 02066641-A 1 29-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1 from Patent WO02066641.
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  /note="exon A"
2108. .2125
                                                                                                                                                                                               1980. .1998
/note="5-390-177.mis"
                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DN
/db_xref="taxon:9606"
                                                                 note="5-390-177.mis"
                                                                                                        note="5-390-177 : polymorphic base"
                                                                                                                                                                                                                                         l823. .1840
/note="5-390.pu"
                                                                                                                                                       bound_moiety="5-390-177.probe"
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<u>.</u>	=	/note="4-58-289 : polymorphic base G or C" 39974, .39992	/bound_moiety="4-58-289.probe" 39973	.39985	.39972		.39963 4-58-318,mis complement"		bound	/note="4-58-318.mis" /note=14-58-318.mis" 39932	/note="4-58.rp" 3992539943	/note="exon T" 3987739896	/note="4-59.rp" 3970440858	/note="exon S" 3955639574	7.00Ce="eXon F" 3737737466	34261. 34404	3135731471 /note="exon E"			/note="5-392-364 : insertion of G"	=	od	. polimownkie base o ou	1027410298 /bound moiety="5-392-280.probe"	/note="5-392-280.mis"	=	/note="5-392-222 : polymorphic base G or T"	٠,-	-	/note="exon C" 1020910227	/note="5-392.pu" 1011510233	1000710025	,	46274718 /note="exon B"	11	/note="5-391-43 : polymorphic base A or G"	/bound_moiety="5-391-43.probe" 4601	/note="5-391-43.mis" 45894613	/noce="5-391.pu" 45824600	/note="5-390.rp complement" 4559. 4577
primer_bind	primer_bind	exon	primer_bind	non	. Diliging		3	primer bind	primer_bind	primer_bind	variation	misc_binding	primer_bind	primer_bind	primer_bind	٠ 'د		e i	misc binding	primer_bind	primer_bind	exon	ı	b. '	primer bind	variation	misc_binding	primer_bind	primer_bind	primer_bind	primer_bind	LOI	Firmita 2	hindi	primer_bind	variation	primer_bind	misc_binding	primer_bind	bin
7100e="0-09/.1p complement" 7585875877	973117		.72857 3-397-141.mis complement"	72838 /note="5-397-141 : polymorphic base G or T"	/bound_moiety="5-397-141.probe"	/note="5-397-141.mis"	/note="5-397.pu" 72819 72817	/note="4-88.pu complement" 7269872715	.69626	porymorphic base a or	4-BB-107 · polymorphic base A	6950969533 /bound_mojetv="4-88-107.probe"	6950269520 /note="4-88-107.mis"		6772467741 /note="99-86.pu complement"	/note="99-86-266.mis complement"	/note= /note="99-86-266 : polymorphic base A or G"	/bound_moiety="99-86-266.probe"	/note="99-86-266.mis" 67463. 67487	67474	6728967309	5043650545 /note="exon G"	/note="4-51.pu complement"	/note="4-51-312.mis complement" 4252642543	<pre>/note="4-51-312 : polymorphic base G or C" 4223342251</pre>	molecy="4-51-312.probe"	.42244	4221342231 /potos="4-51-313 mic"	4212242141 /note="4-51.rp"	.41581 1-54.pu compl	.41423 4-54-180.mi	=	/bound_moiety="4-54-180.probe"	=	1-54-199 : pc ,41404	d Cd FCC EFD	180 mis=	4137341397 /bound_moietv="4-54-199.probe"	4136641384 /note="4-54-199.mis"	4113741154 /note="4-54.rp"

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Matches 545;
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                                                                                                                                                                 CTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCCTAC
                                                                                                                                                                                                                             AATGCCCAGGGGTCCTGTAACAGATCGGTTTTTCCCAGAGGGTTTCTGCAGCATGGGTCC
                                                                                                                                                                                                                                                                                                                     TCAGACAAAAGAGATCAACTGCTCTCTCTAGGAAATACTTAATTGGGGTGGTGCCTAGGA
                                                                                                                                                                                                                                                                                                                                                               ACAGACAACAGAGCCCCA-GCTACTCTCTAGGAAA----TAATTAGGGTGGTGCCTCTGA
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TATCAACTTATCATATAAGGGAAGGAAAGTGATTGATTCGGATACTGACACTGTAGACTC
                                             AGGAAGATAACGGCTAAGCCAGGAGGGGGGGAGCAGCCCACTACACATGTCTGGCTGCTCT
                                                                                                                                                                                                                                                                     CATGCCCAGGGTCTTGTGGCTGGTCTG-TGTTCCCAGAAGGCTTCTGCAGTACACAGTC
                                                                                                                                                                                                                                                                                                                                                                                                          CTTCAACATTAAAGTTATTACCTCAGATATTTTGCCAGCTTAGCACGGCAAAAATCAGTT 158095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCCTGACCTATTTGTAGTATTTTTATTCCTAAAGGAAAAAACAGGAACTTTCATTGTA 158155
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                                                                              AGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCT
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75989. .76151
/note="exon I"
76041. .76059
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81241. .81265
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81006. .81025
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76289. .76306
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76048. .76072
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Pred. No. 2.8e-44;
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                             244 AAGGAAAAGGTGTATGTTTGTTTCCTCTCGACATACTTCACTCAAATATCTATTGTTACT
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Homo sapiens angiopoietin-2 (AGPT2) gene, promoter region, 5' UTR
and partial cds.
AX563557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 6714)
Fiedlar, U., Hegen, A., Augustin, H.G. and Koidl, S.
Direct Submission
Submitted (04-MAR-2004) Vascular Biology and Angiogenesis Research,
Tumor Biology Center Freiburg, Breisacher Str. 117, Freiburg 79106,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression of Angiopoietin-2 in Endothelial Cells is Controlled by Positive and Negative Regulatory Promoter Elements (er) Arterioscler. Thromb. Vasc. Biol. (2004) In press
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Hegen, A., Koidl, S., Weindel, K., Marme, D., Augustin, H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA
/db_xref="taxon:9606"
/chromosome="8"
/map="8p23.1"
                                                                                                                                                      /codon_start=1
/product="anglopoletin-2"
/protein_id="AAT69979.1"
/protein_id="AAT69979.1"
/db_xref="GI:50082538"
/translation="MMQIVFFTLSCDLVLAAAYNNFRKSMDSIGKKQYQVQHGSCSYTFLLPEMDNCRSSSSPYVSNAVQRDAPLEYDDSVQRLQVLENIMENNTQWLMK"
                                                                                                                                                                                                                                                                                                                                     /product="angiopoietin-2"
4428. .4904
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/gene="AGPT2"
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/gene="AGPT2"
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                                                                                                                                                                                        MGC.
Mus musculus
Mus musculus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 2471)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Schuler,G. Klausner,R.D., Collins,F.S., Wagner,L., Schaefer,C.M., Schuler,G. Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K. Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
                                                                                                                                                                                                                                                                              Mus musculus and IMAGE:3494566),
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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BC027216.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCTTATCAACTTATCATATAAGGGAA
                                                                                                                                                                                                                                              GI:20070843
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                                                                                                                                                                                                        (house mouse)
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                                                         N.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can through the I.M.A.G.B. Consortium/LLNL at: http://image.llr
Series: IRAK Plate: 30 Row: b Collumn: 12
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
Tissue Procurement: Filbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortiu
DNA Sequencing by: Baylor College of Medicine Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.
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NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov
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/db_xref="GeneID:11601"
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/db_xref="MGI:1202890"
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DNMKKEMVEIQONVVQNQTAVMIEIGTSLLNQTAAQTRKLTDVEAQVLNQTTRLELQL
LQHSISTNKLEKQILDQTSEINKLQNKNSFLEQKVLDMEGKHSEQLQSMKEQKDELQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="MGC:25292 IMAGE:3494566"
/tissue_type="Mammary tumor metastatized to lung. The arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
                                                                                                                                                                                                                                                                                                                                                                       /note="synonyms: Ang2, Ang-2"
/db_xref="geneID:11601"
/db_xref="MGI:1202890"
238..1728
                                                                                                                                                                                          /codon_start=1
/product="Agpt2_protein"
/protein_id="AAH27216.1"
/db_xref="GI:20070844"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Agpt2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Lu29"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="Czech II"
                                                                                                                                                                                                                                                                                                                              'gene="Agpt2"
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National Cancer
da, MD 20892-2590,
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Mus musculus angiopoietin-2 mRNA,
AF004326
                                                                                                                                                                                                           Direct Submission
Submitted (16-MAY-1997) Discovery,
Old Saw Mill River Rd., Tarrytown,
                                                                                                                                                                                                                                                                                                                                                                                                             Maisompierre, P.C., Suri, C., Jones, P.F., Bartunkova, S., Maisompierre, P.C., Suri, C., Jones, P.F., Bartunkova, S., Wiegand, S.J., Radziejewski, C., Compton, D., Aldrich, T.H., Papdopoulos, N., Daly, T.J., Davis, S., Sato, T.N. and Yancopoulos, G.D. Papdopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
                                                                                                                                                                                                                                                                   2 (bases 1 to 2424)
Maisonpierre, P.C., Suri, C., Jones, P.F., Bartunkova, S.,
Wiegand, S.J., Radziejewski, C., Compton, D., Aldrich, T.H.,
Papdopoulos, N., Daly, T.J., Davis, S., Sato, T.N. and Yancopoulos, G.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Science 277 (5322), 55-60 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                         /mol_type="maxis"
/db_xref="taxon:10090"
/tissue type="uterine"
/clone_Tib="mouse uterine cDNA library (Clontech)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Agpt2"
/note="filament; Region:
/db xref="CDD:pfam00038"
1072. .1719
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EQTTFROLAEIFKSKLTTSGIYTLTFPNSTEEIKAY.COMDVGGGGWTV U QHREDGSVD
FQRTMKEYKEGFGSPLGEYNLGNEFVSQLTGQHRYVLKIQKRWEGNBAHSLVDHFYL
AGEESNYRIHLTGLTGTAGKISSISQPGSDFSTKDSDNDKCICKCSQMLSGGWWFDAC
/note="Ligand for the Tie2/Tek receptor tyrosine kinase;
Method: conceptual translation with partial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Agpt2"
/note="FBG; Region: Fibrinogen-related domains (FReDs)"
                                                                                                                           organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 7e-44;
0; Mismatches
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                                                                                                                                                                                                             Regeneron Pharmaceuticals, NY 10591, USA
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RESULT 11
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CE 1 (bases 1 to 221218)

Peccra; Bovidae; Bovinae; Bos.

CE 1 (bases 1 to 221218)

RS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,

Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,

Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,

Baldwin,D., Bardaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,

Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,

Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,

Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,

Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,

Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,

Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,

Cleveland,C., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,

Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,

Dayado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,

Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,

Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,

Franser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,

Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,

Gunarandez,S., Haladun,S.L., Hodgson,A., Hogues,M.,

Hollins,B., Hawells,S., Hume,J., Idebird,D., Jackson,A.,

Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,

Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
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AGEESNYRIHLTGLTGTAAKISSISQPGSDFSTKDSDNDKCICKCSQMLSGGWWFDAC
GPSNLNGQYYPQKQNTNKFNGIKWYYWKGSGYSLKATTWMIRPADF"
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/product="angiopoietin-2"
/protein_id="AAB63189.1"
/db_xref="GI:2257931"
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Pred. No. 2.2e-38;
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4G DRAFT SEQUENCE,
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27 unordered
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18

f 50 bp g of 3361 bp in length f 50 bp g of 1390 bp in length

bp 43144 bp in length

bp 21510 bp in length bp 4119 bp in length of 2088 bp in length 50 bp of 9758 bp in length

50 bp of 1824 bp in length

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Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Maheshwari, M., Mahindartne, M., Martin, R., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Morris, S., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Nontemayor, J., Moore, S., Milosavljevic, A., Morris, S., Munidasa, M., Murphy, M., Nair, L., Milosavljevic, A., Morris, S., Murphy, M., Nair, L., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nawkelemeh, O., Okwuonu, G., Olarmpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plazzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Sanders, W., Savery, G., Scherer, S., Scotel, G., Shatsman, S., Shen, H., Shetty, J., Shetty, J., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Vilasana, D., Waldron, L., Walker, B., Wang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von, Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weins, R., Smith, D.R., Holt, R.A., Smith, H.O., Weins, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                           * NOTE: Estimated insert size may differ from sequence length
* ____(see_http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 26, 2005 this sequence version replaced gi:58037895.
The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-NOV-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 221218) Cow Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 221218)
                                                                                                 Center project Information
Center project name: FAML
Center clone name: CH240-8B21
Center clone name: CH240-8B21
Center clone name: Atlas 3.0;
Consensus quality: 213012 bases at least Q40
Consensus quality: 215322 bases at least Q30
Consensus quality: 217444 bases at least Q20
Estimated insert size: 214243; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor Co
                                                                                                                                                                                                                                                                                                                                                                      Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Genome Center
     This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Kraft,C.L., Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                   College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lewis, L., Li, Z., Liu, J.,
                                                                                                                                                                                                                                                                                                                   FEATURES
gap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record
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17232
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                                                                                                                                                                                                                                 type="genomic
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length length

bp in length

of 1054 unknown

ni dq

length length

unknown of 1305

length

unknown of 1782

bp in l

in length

bp in length
length

length

bp in length length

50 bp of 7455

bp in length

of 1861 bp unknown

in length

50 bp of 11087 bp in length

Length

50 bp of 20702 bp in length 50 bp of 7266 bp in length 50 bp of 7980 bp in length

ър 35368

bp in length

bp 1158 bp in length bp 7862 bp in length

9187 bp in length

bp 4929 bp in length

8143 bp in length

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HS164G8F
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     H. sapiens CpG island DNA genomic forward read cpg164g8.ftla. Z57119 GI:1028350
                                                         HS164G8F
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                                                                                                                                                                   CACAGT-CCTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGA
                                                                                                                                                                                                                                                                                                                                                 CCTCTGACATGCCCAGGGGTCTTGTGGCTGGTTGTGTTTTCCCAGAAGGCTTCTGCAGTA
                                                                                                                                                                                                                                                                                                                                                                             TCAGTTTCAGACACAGGAGACCTACAGGCTCTCTCTAGGAAACAGTCAATTAGGGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                GAACTTTCATTGTACTTTAAAGCTATTGCCCCAGATATTTACCAGCTTCGCGCTGTGAAA
                                                                                                                    TGCAGAATCTGGGGAAGAGAGAGACAAAGCAGCGCTAAC 141391
                                                                                                                                                                                                                      CCCCCTACAGGAAGATAACGGGCAAGCCGGAGGGGGAGCCGCCGGCTGCACATGTCT
                                                                                                                                                                                                                                      -CCCCCTACAGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGGTGGCTGCACATGTCT
                                                                                                                                                                                                                                                                        TATAGTCCCGGTTGGACAGTACACATCAAGCCCGGATTTTTCCTGTGGCCTGGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCTTGGAA---AAGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTTACAATAAAG
                                                                                                                                            TGTAGACTCAGGGGAGAAACAAAGAGTCCGTGCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAATAAACCAAGGTCCCGATATA----GCTGTAATTTTATTCCTAAAAAGAACAGAAAACTT
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Pred. No. 2.4e-33;
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Homo sapiens
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llarity 81.9%;
Conservative
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/clone_lib="CGI-1"
/dev_stage="adult"
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944 GGATACTGACACTGTAGACTCAGGGGAGAAACAAAGA
Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Emammalia; Eutheria; Euarchontoglires; Glires; Rodenti Sciurognathi; Muroidea; Muridae; Murinae; Rattus. 1 (bases 1 to 132392) 1 (bases 1, Metzker, M.Lee., Abramzon, S., Adams, C.
                                                                                                                                               AC141003.1 GI:28875862
HTG; HTGS_PHASE1.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.
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Dodsworth, S.J., Huckle, E., Wilkinson, P. and Micklem, G.
Dotsworth, S.J.
Direct Submission
Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P Purification of CpG islands using a methylated Nat. Genet. 6 (3), 236-244 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATACTGACACTGTAGGATCTGGGGAGAGAGGGAACA
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Pred. No. 7.5e-30;
0; Mismatches 48
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Gebregorgis, E., Geer, K., Gill, R., Grady, M., Gebera, W., Goles, M., Jackson, J., Jackson, J., Jackson, J., Johnson, R., Jolkes, M., Jackson, J., Lawis, J., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
Direct Submission
Submitted (07-MAR-2003) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Paylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Center: Baylor Collège of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GXKS
Center clone name: CH230-526115
Center clone rame: Prabatics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
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COMMENT

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will Consensus quality: 98530 bases at least Q40 Consensus quality: 105678 bases at least Q30 Consensus quality: 110755 bases at least Q20 Estimated insert size: 86014; sum-of-contigs estimation Quality coverage: 1x in Q20 bases; sum-of-contigs estimation

as soon as it be preserved.

9070 9170 10302 10402 114938 112038 113407 113507 114991 115091 115091 115091 117286 117286 117386 117386 36003 36103 37500 30549 31895 31995 33379 33479 34876 34876 20895 22417 22517 23640 23740 23740 24843 24943 26029 26029 26129 27719 27819 29222 29322 5659 6672 6772 7850 1019 1119 2165 36002: 36102: 37499: 34875: 31894: 31994: 26128: 27718: 24842: 18963 30448: 9069 9169 10301 16107 20894 1018: 1118: 2164: contig gap of contig contig gap of contig unknown of 1590 unknown of 1403 unknown of 1078 unknown of 1578 unknown of 1013 unknown unknown of 1127 of 1103 unknown of 1123 unknown of 1017 unknown of 1484 unknown of 1078 of 1076 unknown of 1384 unknown of 1086 unknown of 1522 of 1731 unknown of 1369 of 1536 unknown of 1132 of 1120 unknown of 1013 of 1005 of 1046 of 1018 bp in length unknown length unknown unknown bp in length
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                                                                                                     Homo sapiens partial mRNA for angiopo AJ289781
AJ289781
AJ289781.1 GI:10120297
angiopoietin-2 gene; angiopoietin-2A.
Homo sapiens (human)
Homo sapiens
                 Wezquita,J., Mezquita,P., Montserrat,P., Vilagrasa,X. and Mezquita,C. Genomic structure and alternative splicir angiopoietin-2
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                       lominidae;
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     Biophys. Res. Commun.
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AX458641
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Sequence 187 from Patent
AX458641
AX458641.1 GI:21725305
                                                                                                 Epigenomics AG (DE)
                                                                                                         Diagnosis of diseases associated with angiogenesis Patent: WO 0246454-A 187 13-JUN-2002;
                                                                                                                                                                   synthetic construct synthetic construct other sequences; artificial sequences.
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                                                                                                                                              Schacht, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUN-2000) Mezquita C., p) University of Barcelona, Casanova 143, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mezquita, C
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                    /organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
                                                                       1. .2846
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/product="angiopoietin-2a"
/protein_id="CatoB180.1"
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          note="chemically
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476. .>763
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/mol_type="mRNA"
/db_xref="taxon:9606"
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76.7%;
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Pred. No. 2.6e-22;
D; Mismatches 56
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Best Local Similarity 62.1%; Pred. No. 1.1e-21; Matches 295; Conservative 0; Mismatches 164; Indels 16; Gaps 4; Oy 522 ATCITAGCCTITATATTITACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATT 581 Db 1530 ATTITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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Listing first 45 s
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N_Geneseq_21:*
1: geneseqn1980;
2: geneseqn2090;
3: geneseqn2000;
4: geneseqn2001;
6: geneseqn2002;
6: geneseqn2002;
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8: geneseqn2003;
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Copyright (c) 1993 - 2005 Compugen Ltd.
 geneseqn2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 19 !	C 18	c 17	c 16	c 15	C 14	c 13 1:		11 1	_	9 2	8	7	σ	ი 5	0 4	G	N	.	;	Result
51.6	51.6	52.6	54.4	55	58	39.4	40.6	143.4	156.6	11.8	213	213	213	238	238	238	276		Score M	0
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ADE84216	ABN80121	ADW10467	ABL34141	ABL32893	ADA71938	ABQ67158	ABQ67157	ADD69421	ABX63024	ADQ09371	ADU39008	ADS13802	ADQ09378	ABQ81802	AAF24497	ADD69391	ADZ61847	AD043367	ID	
Ade84216 Human lym	Abn80121 Human che	Adw10467 Colon pro	Abl34141 Human imm	Abl32893 Human imm	Ada71938 Rice gene	Abq67158 Human ang	Abq67157 Human ang	Add69421 Human Ang	Abx63024 Human cDN	Adq09371 Human Ang	Adu39008 Mouse Ang	Ads13802 Mouse ang	Adq09378 Murine An	Abg81802 Human PG-	Aaf24497 Human PG-	Add69391 Human PG-	Adz61847 Murine Ag	Ado43367 Mouse Ang	Description	

Disclosure; SEQ ID NO 1; 69pp; English.

angiogenesis.

New polynucleotide comprising a first nucleic acid encoding a light-generating gene product and a second nucleic acid encoding a selectable marker, useful in identifying a compound capable of modulating

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48.4	48.4	48.4	48.6	49	49	49	49	49	49	49	49.2	49.8	50	50	50	50	50.2	50.8	50.8	51.2	51.2	51.6	51.6	51.6	51.6
0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2
4661	4661	4661	487	8900	8900	8758	6127	6127	6127	2000	13784	15479	4415	4415	4415	4415	9964	6101	6101	20486	20486	6823	6523	6523	6523
J)	თ	თ	φ	13	13	σ	7	σ	σ	11	σ	σ	7	6	6	0	σ	13	13	7	σ	σ	13	13	10
AAS61136	ABL70185	ABK31226	ACH18710	ADS89411	ADS89685	ABL33118	ADS99710	ABL70120	ABL34449	ACL37108	ABK40062	ABK39964	ADS99863	ABL70423	ABL34602	ABL33906	ABL32099	ADS89416	ADS89690	ADS99872	ABL34611	ABL33144	ADS89346	ADS89620	ADE84140
Aas61136 Human gen		Abk31226 Signal tr	Ach18710 Human adu	Ads89411 Oligonucl	Ads89685 Oligonucl	Abl33118 Human imm	Ads99710 Complemen	Ab170120 Chemicall	Abl34449 Human met	Acl37108 Rice stre	Abk40062 Human che	Abk39964 Human che		Ab170423 Chemicall	Abl34602 Human met	Abl33906 Human imm	***	Ads89416 Oligonucl	Ads89690 Oligonucl	Ads99872 Complemen	Abl34611 Human met	Abl33144 Human imm	Ads89346 Oligonucl	Ads89620 Oligonucl	Ade84140 Human lym

ALIGNMENTS

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key Location/Qualifiers prim_transcript 1008. .1220
                                                                                                                                                                                                               Mus sp.
                                                         WPI; 2004-365502/34.
                                                                       Livingston
                                                                                                    25-JUL-2002; 2002US-0398583P.
24-JUL-2003; 2003US-00627075.
                                                                                                                                         06-MAY-2004.
                                                                                                                                                                                                                              Ang-2; enhancer; mouse; cell imaging; antiangiogenic;
                                                                                                                                                                                                                                            Mouse Ang-2 cis-acting regulatory sequence.
                                                                                                                                                                                                                                                                          ADO43367;
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                                                                                                                         25-JUL-2003; 2003WO-US023152
                                                                                                                                                       WO2004037975-A2.
                                                                                                                                                                                                                                                            29-JUL-2004
                                                                                      (DAND ) DANA FARBER CANCER INST INC.
                                                                      DM,
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                                                                       Kung
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/note= "Includes translation initiation codon at 3′ end"
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CC The present sequence is that of the cis-acting regulatory region of the CC murine Ang-2 gene located 5' to the start of transcription. This ciscacting DNA regulates preferential expression in endothelial muscle cells of a polypeptide-encoding DNA to which it is operably linked. The CC invention provides compositions that include a polynucleotide encoding a creporter gene (e.g. a light-generating moiety), a polynucleotide encoding a creporter gene (e.g. a light-generating moiety), a polynucleotide encoding composition is a selectable marker (e.g. an antibiotic) and optionally a regulatory composition of provide encoding a composition is a polynucleotide encoding a composition in the ability to effect transcription of operably linked composition is used for imaging composition in endothelial cells). The composition is used for imaging composition is need to provide a portion of case to be cells. The cells may be healthy cells or tumour cells, in which case composition is used for imaging composition of provided by composition of provided by composition of provided by composition of provided are vectors comprising the polynucleotides, cells (e.g. primary cells, cells from established cell lines, or tumour cells) comprising the production. The transgenic animals are used in methods for their cell dentification of a compound capable of modulating angiogenesis or which can be continued to be composed to the cells in methods for the cell dentification of a compound capable of modulating angiogenesis or which can be continued to pathway.
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                                                                                            fusion protein; fibrinogen-like; coiled-like domain; angiopoletin-related factor; ARF; angiopoletin; Ang-1; Ang-2; Ang-3; Ang-4; Ang-2X; vulnerary; antinfilammatory; vasotropic; necrosis; ischaemia; inflammation; wound healing; CCD; FLD; human; PG-3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a methods for screening biologically active agents, such as candidate drugs, to determine whether the agent possesses a defined biological activity. The methods involve making one or more comparisons chosen from comparing efficacy value of agent to reference efficacy value, comparing a toxicity value of the agent to reference toxicity value, comparing a classifier value of the agent to
                                                                                                                                                                                                                                                                         Human PG-3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD69391 standard; DNA; 240823 BP
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Pred. No. 2.4e-62
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identical or homologous to that of an angiopoietin-related factor (ARF), examples of which include Ang (angiopoietin)-1, Ang-2, Ang-3, Ang-4 and Ang-2X. The molecules of the invention demonstrate vulnerary, antiinflammatory and vasotropic activities whilst the fusion protein may be useful for preparing a composition for treating necrosis, ischaemia or inflammation, as well as for promoting wound healing. The current sequence is that of the human PG-3 DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein comprising a fibrinogen-like or coiled-like domain, useful for preparing a composition for treating necrosis, ischemia or inflammation, or for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 240823 BP; 66383 A; 50394 C; 51548 G; 72418 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel fusion protein comprising a fib-
like domain (FLD) or coiled-coil domain (CCD). The domain may be
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                                ACAGACAACAGAGCCCCA-GCTACTCTCTAGGAAA----TAATTAGGGTGGTGCCTCTGA
                                                                                                                                                                                                                       GCACACGTTTACAGGAGCCAAACTTCTTCCTCTTTATTTGTAATAACAAAAATAAACCGA
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TCAGACAAAAGAGATCAACTGCTCTCTCTAGGAAATACTTAATTGGGGTGGTGCCTAGGA
                                                                     CTTCAACATTAAAGTTATTACCTCAGATATTTTGCCAGCTTAGCACGGCAAAAATCAGTT
                                                                                                      CTTTAAAATTTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGCCTACAAACGAGCAG--
                                                                                                                                               AGTCCTGACCTATTTGTAGTATTTTTATTCCTAAAGGAAAAAACAGGAACTTTCATTGTA
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Pred. No. 2.1e-51;
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/*cag= 1 /note= " binds probe" replace(4601,G) /*tag= m complement(46024620) /*tag= n	/*tag= j /*tag= j 45824600 /*tag= k 45894613	in vi	/*tag= t 2001. 238825 /*tag= g /product= "PG-3" /note= "this sequence contains introns"	/note= "binds probe" replace(1999,C) /*tag= e /complement(20002018)	V) H	/*tag= a /note= "5' regulatory region" 1823. 1840 /*tag= h	Location/Qualifiers 12000	ancer; BRCA1; chromosome 8p23; ds.	ie.	(first entry)	tandard; cDNA; 240825 BP.	GACAGC 1032 AGTGAGC 157725	AGGGAGAACAAAGAGTCCGTGCAGACCTCTGGAGTGAGCAGGGCTGCTCCTTCCT	TCAACTTATCATATAAGGGAAGGAAAGTGATTGATTCGGATACTGACACTGTAGACTC 964 	AGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCT 904	CTTTGGGGCAGTAAGCACTATGCTCTGATTTTCCTGTTGCCTGGCTAGTGACCCCCTAC 845	AATGCCCAGGGTCCTGTAACAGATCGGTTTTTTCCCAAGACCGTTTTTTTCCCAGGGTCCTGTAACAGATCGGTTTTTTTCCCAAGACCGTTTTTTTCCCAGACGGTTCTTTTTTCCAGACGGTTCTTTTTTCCAGACGGTTCTTTTTTTCCAGACGGTTCTTTTTTTCCAGACGGTTCTTTTTTTCCAGACGGTTCTTTTTTTCCAGACGGTTTTTTTT
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replace(39973,C) /*tag= aq /*tag= ar /*tag= ar /*tag= ar /*tag= ar 4024240259 /*tag= as	/*tag= an 3995439972 /*tag= ao 3996139985 /*tag= ap	. 7 "	/*tag= aj 3993239956 /*tag= ak /note= "binds probe"		/label= S 3955639574 /*tag= ah 39704. 40858	/*Cag= ae /label= F 37377. 37466 /*tag= af			1041110430 /*tag= ab 2681026897		/notes		/note= " binds probe" replace(10228,T) /*tag= u /*tg= u complement(1022910247)	1020910227 /*tag= s 1021610240 /*tag= t	".		46274718

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Gaps

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/reag= by//note="binds probe"
replace(72838,T)
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/*tag= bp

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/label= g

67289. 67309

/*tag= bk

67456. .67474

/*tag= bl
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41564.
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/*tag= bu
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/note= "_binds_probe"
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                                                                 TGGGGAGAGAGGAACAAAGGACCGTGAAAGCTGCTCTGTAAAAGCTGACACAGCCCTCCC 157735
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72881. .72918
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73099. .73117
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/4582. 4600
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10209.
/*tag=
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/standard_name= "single nucleotide polymorphism
/note= "polymorphic base A or G; the nucleotide
as an IUPAC ambiguity code in the specification"
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/number= 2
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/*tag= ad grame= "single nucleotide polymorphism (SNP)"
/note= "polymorphic base G or C; the nucleotide is give
/note= "polymorphic code in the specification"
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39925.
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as an IUPAC ambiguity code in the specification"
complement(39945. .39963)
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39932.
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34261. .34404
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complement(10287. .10305)
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/note= "polymorphic base G or T; the nucleotide i
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                                                                               TATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTG
                                    ANATTCTAATTTCTCTATTGTAATGTAATGAACTTAATCAGTACAGTGTATTTTTAGAGT
                                                  TCACTCAAATATCTATTGTTACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTT
                                                                 CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGTTTGTATTCCTCTTTCTACACAGACACTT
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/standard_name= "single nucleotide polymorphism (S)
/note= "polymorphic base A or C; the nucleotide is
as an IUPAC ambiguity code in the specification"
complement (41386. .41404)
/*tag= ee
41392. .41416
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= aj
/standard_name= "single nucleotide polymorphism
/note= "polymorphic base G or C; the nucleotide :
as an IUPAC ambiguity code in the specification"
complement (39974. .39992)
/*tag= dz
                                                                                                                                         /note=
42232
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/standard_name= "single nucleotide polymorphism (
/note= "polymorphic base A or C; the nucleotide /
as an IUPAC ambiguity code in the specification"
complement(41405. .41423)
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/*tag= ef
complement (41564.
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64.3%; Pred. No. 2.1e-51;
vative 0; Mismatches 265;
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RESULT 6
ADQ09378
ID ADQ0
                                                                                CDS
                                                                                                                                                                                  Mouse; Angiopoietin-2; gene; ds; antisense oligonucleotide; phosphorothioate linkage; 2'.-O-methoxyethyl sugar moiety; 5-methylcytosine; hyperproliferative disorder; cancer; cyto
                                                                                                                                                                                                                                                                     Murine Angiopoietin-2
                                                                                                                                             Mus musculus.
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US2004115640-A1
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211. .1701
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                                       "Murine Angiopoietin-2"
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Best Local Similarity
Matches 213; Conserv
                                                                        Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic; antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a compound targeted to a nucleic acid molecule encoding the human Angiopoietin-2 polypeptide. The compound is an acid and inhibits expression of the polypeptide. The antisense cligonucleotide that specifically hybridises with the nucleic oligonucleotide expression of the polypeptide. The antisense i.e. a phosphorothicate linkage, at least one modified sugar moiety, preferably a 2.0-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methyloytosine. The antisense compounds are useful for modulating the expression of the human Angiopoietin-2 polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents DNA encoding the murine Angiopoietin-2 polypeptide of the invention.
  CDS
                                           BUM
                                                                                                                      Mouse angiopoietin-2 (Ang-2) encoding
                                                                                                                                                        02-DEC-2004
                                                                                                                                                                                                           ADS13802 standard; DNA; 2424 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligonucleotide compound that inhibits expression of Angiopoietin-2, useful for preparing a composition for treating hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13;
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GENBANK; AF004326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-449380/42.
P-PSDB; ADQ09609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder, e.g., cancer.
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                                                                 therapy; mouse; gene; Ang-2; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2424 BP; 709 A; 581 C; 625 G; 508 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Location/Qualifiers 211. .1701
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Pred. No. 1.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 34; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-653413/63
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                                                                                                                                                                                                                                               1008 GGCTGCTCCTTCCTCAGGACAGCTCCGAGTGTGCCGGGGAGAAGAGAAAGAGAAGAGAGAC
                                                                                                                                                              1068 AGGCACTGGGAAAGAGCCTGCTGCGGGACGAGAAGGCTCTCACTGATGGACTTATTCAC
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CACAGTTTAGAACCCAAAAAGAGAGAGAGAATG
                                                                          ACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAGAGCTCAGGACGCAAGTTTGCTGAACT 1187
                                                                                                                                                                                                                     GGCTGCTCCTCTCAGGACAGCTCCGAGTGTGCCGGGGAGAAGAGAAGAAGAAGAGAC
                                                                                                                               AGGCACTGGGAAAGAGCCTGCTGCGGGACGGAGAAGGCTCTCACTGATGGACTTATTCAC
                                         ACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAGAGCTCAGGACGCAAGTTTGCTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                         2424 BP;
                                                                                                                                                                                                                                                                                                                ilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                  709 A; 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "Ang-2"
                                                                                                                                                                                                                                                                                                                                17.5%; Score 213; DB 13; 100.0%; Pred. No. 1.2e-45;
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  1220
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sease, or
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180

120 1127 60 1067 0

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밁
 181
CACAGTTTAGAACCCAAAAAGAGAGAGAGAGAATG 213
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ADU39008; ADU39008 standard; cDNA; 2424 ВP

27-JAN-2005

(first

small interfering RNA; siRNA; Angl; Ang2; Tie2; angiogenesis; inhibito type I diabetes; antiangiogenic; cytostatic; antidiabetic; optothalmological; nephrotropic; neuroprotective; cardiant; vasotropic; gene therapy; cholesterol; endometrial neovascularisation; tumour; Mouse Ang2 cDNA retinopathy; age-related macular degeneration; gene; ss. Tie2; angiogenesis; inhibitor;

Mus musculus

WO2004094606-A2

04-NOV-2004

19-APR-2004; 2004WO-US012072

18-APR-2003; 2003US-0463981P

(UYPE-) UNIV PENNSYLVANIA.

Reich SJ,

Tolentino

2004-795558/78

and an antisense RNA strand, useful for treating angiogenic diabetic retinopathy or age-related macular degeneration. New isolated small interfering RNA (siRNA) comprising a sense RNA strand and an antisense RNA strand, useful for treating angiogenic disease, e.g e.g.

Claim 2; SEQ ID NO 5; 182pp; English

CC comprises a nucleotide sequence substantially identical to a target CC sequence of 19-25 contiguous nucleotides in human Angl. Ang2 or Tie2 mRNA, or an alternative splice form, mutant or cognate. The invention CC further comprises: a recombinant plasmid comprising nucleic acid sequences for expressing an siRNA comprising a sense RNA strand and an CC antisense RNA strand; a recombinant viral vector comprising nucleic acid sequences for expressing an siRNA comprising a sense RNA strand and an CC antisense RNA strand; a pharmaceutical composition comprising siRNA, the plasmid, or the viral vector and a pharmaceutical carrier; a method of inhibiting expression of human Ang1, Ang2 or Tie2 mRNA, or an alternative splice form, mutant, or cognate; a method of inhibiting angiogenesis in a subject; a method of treating an angiogenic disease in a subject; and a method of treating an angiogenic form type I diabetes in a cc subject. The siRNA oligos have the following activities: antiangiogenic, cytostatic, antidiabetic, ophthalmological, nephrotropic. The subject; and an angiogenesis in a subject. The angiogenesis is pathogenic angiogenesis in a subject. The angiogenesis is pathogenic or non-pathogenic. The non-pathogenic angiogenesis or cholesterol production. The non-pathogenic angiogenesis comprises a tumour associated with a cancer selected from breast cancer, lung cancer, head cancer, pastnormal cancer, colon cancer, concerdad cand neck cancer, neuroblastoma, osteosarcoma, ovarian cancer, pancreatic concerned cancer, prostate cancer, gastrointestinal cancer, glioma, liver cancer, comprises endication arising of from type I diabetes in a cubicar conservation. Treating composition cancer arising concernation. Treating concernation cancer arising concernation. Treating concernation cancer arising concernation cancer arising concernation. Treating concernation cancer aris comprises a sense RNA strand and an antisense RNA strand. The sense antisense RNA strands form an RNA duplex, where the sense RNA strand comprises a nucleotide sequence substantially identical to a target complications arising from type I diabetes in a subject comprises The invention relates to a novel isolated small interfering RNA (siRNA) and

The invention relates to a compound targeted to a nucleic acid molecule encoding the human Angiopoietin-2 polypeptide. The compound is an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage

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RESULT 9
ADQ09371
ID ADQ0
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XX Huma
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                                                                                                                                                                                                                      disorder,
                                                                                                                                                                                                                                            New oligonucleotide compound that inhibits expression of Angiopoietin-2, useful for preparing a composition for treating hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                     Myers K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-2002; 2002US-00317803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Angiopoietin-2; gene; ds; antisense oligonucleotide; phosphorothioate linkage; 2'.O-methoxyethyl sugar moiety;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Angiopoietin-2 DNA #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ09371 standard;
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                                                                                                                                                               Claim 1; SEQ ID NO 4; 102pp;
                                                                                                                                                                                                                                                                                                                               WPI; 2004-449380/42.
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Best Local S
Matches 335
28-JUL-2000;
08-JAN-2001;
                                                                                                                                                 hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
                                                                                                                     Homo
                                       08-JAN-2002;
                                                                                          US2002137081-A1
                                                                                                                                                                                               Human; gene;
                                                                                                                                                                                                                      Human cDNA #24 differentially expressed
                                                                                                                                                                                                                                                    25-FEB-2003
                                                                                                                                                                                                                                                                                                     ABX63024 standard; cDNA; 3251
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                                                                                                                                                                                                                                                                                                                                                                                            GAGCAGGGCTGCTCCTCTCAGGACAGC 1032
                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGATACTGACACTGTAGGATCTGGGGAGAGAGGAACAAAGGACCGTGAAAGCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGATACTGACACTGTAGACTCAGGGGAGAACAAAGAGTCCGTGCAGACCTCTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGCCTGGCTAGTGACCCCCTACAGGAAGATAACGGCTAAGCCAGGAGGGGGGGAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCCTGGCTAGTGACCCCCTACAGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGGTTTCTGCAGCATGGGTCCTGGTTGGAGGCAGGCATTCTGCTCTGATTTTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGGCTTCTGCAGTACACAGTCCTTTGGGGCCAGTAAGCACTATGCTCTGATTTTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTAATTGGGGTGGTGCCTAGGAAATGCCCAAGGGTCCTGTAACAGATCGGTTTTTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --TAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTAGCCTACAAACGAGCAG--ACAGACAACAGAGCCCCA-GCTACTCTCTAGGAAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGAACAGAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAACAGGAACTTTCATTGTACTTCAACATTAAAGTTATTACCTCAGATATTTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62705 BP; 19403 A; 12918 C; 12719 G; 17665 T; 0 U; 0 Other;
2000US-0222469P.
2001US-0260483P.
                                       2002US-00044090
                                                                                                                                                                                       ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%;
74.3%;
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                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 211.8; DE Pred. No. 1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 107;
                                                                                                                                                                                                                    in activated vascular
                                                                                                                                                                                                                                                                                                                                                                    481
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                                                                                                                                                                                                                   tissue.
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This invention relates to a combination comprising several cDNAs that are CC discloses a high throughput method for detecting differentially expressed convas in a sample. The cDNAs of the invention may have antiatreriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic; cytostatics and cerebroprotective activities and may be used in a high-cytostatic and cerebroprotective activities and may be used in a high-cytostatic and cerebroprotective activities and may be used in a high-cytostatic and cerebroprotective activities and high-cytostatic and cerebroprotective activities and high-cytostatic and cerebroprotective activities and high-cytostatic and collaborate and collaborate activity a
Sequence 3251 BP; 1083 A; 645 C; 674 G; 849 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activate vascular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-110597/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
U; 0 Other;
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Matches Best Local 192 132 934 874 815 209; 72 12 Similarity GAGCAGCCCACTACACATGTCTGGCTGCTCTTATCAACTTATCATATAAGGAAAGGAAAG TGATTGATTCGGATACTGACACTGTAGGATCTGGGGAGAGAAGAACAAAGGACCGTGAAA TGATTGATTCGGATACTGACACTGTAGACTCAGGGGAGAAACAAAGAGTCCGTGCAGACC TTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGGAAGATAACGGCTAAGCCAGGAGGGCG TTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGGAAGATAGTGGGTGAGCCAGG-GGGCG TGTTCCCAGAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTATGCTCTGAT Conservative 74.9%; ,. Score 156.6; DB 8; Pred. No. 1.2e-30; Mismatches 69; Indels <u>,</u>

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Query Match

12.8%;

Length 3251;

Gaps

RESULT 1: ADD69421 ID ADD6

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TCTGGAGTGAGCAGGGCTGCTCCTTCCTCAGGACAGC

1032 290

> 251 993

933 191

131 873 71 814

GCTGCTCTGTAAAAGCTGACACAGCCCTCCCAAGTGAGC

252

ADD69421 standard; DNA; 763

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RESULT 12
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Best Local S
Matches 188
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like domain (FLD) or coiled-coil domain (CCD). The domain may be
identical or homologous to that of an angiopoietin-related factor (ARF),
examples of which include Ang (angiopoietin)-1, Ang-2, Ang-3, Ang-4 and
Ang-2X. The molecules of the invention demonstrate vulnerary,
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiopoietin-related factor; ARF; angiopoietin; Ang-1; Ang-2; Ang-3;
Ang-4; Ang-2X; vulnerary; antiinflammatory; vasotropic; necrosis;
ischaemia; inflammation; wound healing; CCD; FLD; human; ds; Ang-2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory and vasotropic activities whilst the fusion protein may be useful for preparing a composition for treating necrosis, ischaemia or inflammation, as well as for promoting wound healing. The current sequence is that of the human Ang-2A DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 157; 340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New fusion protein comprising a fibrinogen-like or coiled-like domain, useful for preparing a composition for treating necrosis, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003048185-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-2001; 2001US-0334488P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein; fibrinogen-like; coiled-like domain;
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                                                                                                                                                                                                                                                                     849
                                                                                                                                                                                                                                                                                                                               789 TGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGG
                                                                                                                                                                                                                                                                                                                                                             188;
                                                                                                                                                                                                                                       65
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                        TGAGC
                                                                                                                                            CAACTTATCATATAAGGAAAGGAAAGTGATTGATTCGGATACTGACACTGTAGGATCTGG
                                                                                                                                                                                                      CAACTTATCATATAAGGGAAGGAAAGTGATTGATTCGGATACTGACACTGTAGACTCAGG
                                                                                                                                                                                                                                       AAGATAACGGCTAAGCCAGGAGGGCGGAGCCCCACTACACATGTCTGGCTGCTTTAT
                                                                                                                                                                                                                                                                   AAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGCCACATGTCTGGCTGCTCTTAT
                                                                                                                                                                                                                                                                                                 TTGGAGGGCAGGCATTCTGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCCTACAGG
                                                                                                                   GGAGAGAGGAACAAAGGACCGTGAAAAGCTGCTCTGTAAAAAGCTGACACAGCCCCTCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preparing a composition for treation, or for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                             Conservative
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76.7%;
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Score 143.4;
Pred. No. 2e
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2e-27;
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                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     0 Other;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (I baving sequences (ABG66971-ABG67178) or their complements (I), also related oligomers, are used to evaluate the methylation status and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                        Sequence 2846 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-2000; 2000DE-01061338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; ds.
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748 TGGTCTG-TGTTCCCAGAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-500450/53.
                                                                                                                                                                                                   582 TTATTCCT-
                                                                                                                                                                                                                                                                                             295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; SEQ ID NO 187; 41pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIGENOMICS
                                                                                                                                                                                                                                                                                                           Similarity
                                                TTTTTTTAGGAÄATÄTTTÄÄTTGGGGTGGTGTTTAGGÄÄÄTGTTTAGGGGGTTTTGTAAT
                                                                                                        TTTAGATATTTTGTTAGTTTAGTACGGTAAAAATTAGTTTTAGATAAAAGAGATTAATTG
                                                                                                                                      ATCTTAGCCTTTATATTTACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATT
                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                      -----aaaagaacagaaactttcactatgctttaaaattaaagtgattac
                                                                                                                                                                                                                                                                                                                                                      871 A; 45 C; 651 G; 1279 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated
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                                                                                                                                                                                                                                                                                                         11.5%;
                                                                           - AGGAAATAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGC
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                         Score 140.6; DB Pred. No. 2e-26; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                             164;
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                                                                                                                                                                                                                                                                                                                         Length 2846;
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RESULT 13
ABQ671189/c
ID ABQ671
XX ABQ671
XX ABQ671
XX ABQ671
XX ABQ671
XX Human;
XX Human;
XX Human;
XX Human;
XX Antiar
XX Antiar
XX Antiar
XX Homo 8
PN W02002
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                                                                                                                                                                                   diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, disherin retinomathy magnilar degeneration canada by neovasculariestics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
diagnosis or treatment of cancer.
                                                                                                                                                       Sequence 2846 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-2002
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                                                                                                                                               759 A; 45 C; 565 G; 1477 T; 0 U;
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                                                  Score 139.4; DB 6;
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                            TGACACTGTAGACTCAGGGGAGAAACAAAGA 980
                                                           CTAATAACCCCCTACAAAAAAATAACGACTAAACCAAAAAAACGAAACAACCCACTACAC
                                                                                                                                                       CTAGTGACCCCCTACAGGAAGATAGTGGGTGAGCC-AGGGGGGGGGAGCGGCTGGCTGCAC
                                                                                                                                                                                     CTACAACATAATCCTAATTAAAAAACAACATTCTACTCTAATTTTTCCTATTACCTAA
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RESULT 14
ADA71938/c
ID ADA71938 standard; DNA; 2000 BP.

XX
AC ADA71938;
XY
DT 20-NOV-2003 (first entry)
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DE Rice gene, SEQ ID 5263.
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VX
DE Rice gene, SEQ ID 5263.
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VX
Plant; bacterial infection; fungal infection; viral infection;
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SOS Oryza sativa.
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant pacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2000 BP; 336 A; 265 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2001; 2001WO-IB001105
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                                                    MWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKG
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                                                                                                          KRAKRSYRYRRRWYWKRKGWTYRYRYWRSCRMTRARMSKRRKWAGASMKSCWMYWRGARS
                                                                                                                                                                KKYATRYYWKMWAMTWWWSWRRWKSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARWT
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RESULT 15 ABL32893/c ID ABL32893

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Query Match
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Matches 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10710 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer s disease, Alzheimer, s disease, and inflammatory, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory, vulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 866;
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01-SEP-2000;
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TAAAAAAATGTGCATAACTTAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCC
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAR	
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Result No.	Score	ery tch	Length 699	5 B	ID BY716819	Description
2	276	22.6	24	4	AK019860	AK019860
ω	274.4	L 3		7	CN539462	CN539462
4	263	21.6	330	N	BB847613	BB84761
ហ	253	20.7	354	ᆫ	AA389106	AA389106
6	242	9	2443	4	AK048622	AK04862
7	240.4	19.7	299	N	BB649745	BB649745
8	217.8	17.9	912	N	BE306402	BE306402
9	208.6	17.1	276	N	BB569161	BB569161
10	204	16.7	665	N	BB612537	BB612537
11	203.4	16.7	661	9	AZ984331	AZ984331
12	185.8	15.2	793	11	CR905089	CR905089 Sus scrof
13	178.6	14.6	726	ഗ	BX506958	BX506958
14	175.8	14.4	204	N	BB601394	BB601394
15	167.8	13.8	525	ഗ	BU580281	BU580281
16	149	12.2	921	σ	CB203297	CB203297
17	143.4	11.8	482	œ	DN994582	DN99458
18	133.6	11.0	477	ຎ	BE292322	BE29232
19	133.2	10.9	592	w	BP320006	BP320006
20	٠	10.0	466	თ	CB548076	CB54807
21	119.6	9.8	679	N	BB614741	BB61474
22	93.8	7.7	247	v	BF085046	BF085046

ALIGNMENTS

TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BY716819 LOCUS DEFINITION
Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Batsalov, S., Beised, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaatserland, T., Gariboldi, M., Gisei, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawasawa, Y., Kedzierski, R. M., King, B.L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Munata, K., Okido, T., Pavan, W.J., Pertea, G., Pessole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Satheider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdalle, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wallson, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Mirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakai, K., Sasaki, D., Shibata, K., Sakai, M., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shinagawa, A., Satai, K., Sasaki, D., Shibata, K., Shinagawa, Shinag	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murine; Mus. 1 (bases 1 to 699) (bases	ovary and uterus Mus musculus cDNA clone 5031400E18 5', mRNA sequence. BY716819 BY716819.1 GI:27129936 EST. Mus musculus (house mouse) Mus musculus (house mouse)	linear days pregna

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945 GATACTGACACTGTAGACTCAGGGGAGAAACAAAGAGTCCGTGCAGACCTCTGGAGTGAG 1004
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bmail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashiaume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,J., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Warata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                      Conservative
                                                                                                                                                                 /clone lib="RIKEN full-length enriched, 11 days pregnant adult female ovary and uterus"
/note="Site 1: Sail; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primed [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="ovary and uterus"
/dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="5031400E18"
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100.0%; Pr
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                                         Score 276; DB 5; Pred. No. 1.7e-58;
                                                                                      Length 699
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Nature 420, 563-573 (2002)
6 (bases 1 to 2475)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., /
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., /
                                                                                                                                        Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                    The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                 Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                          Nature 409,
                                                                                                                                                                                                                                                                                                                                              FANTOM Consortium.
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High-efficiency full-length cDNA cloning
Math. Enzymol. 303, 19-44 (1999)
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AK019860
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                                  Arai, A.,
Fukunishi
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Query Match 22.6%; Score 276; DB 4; Best Local Similarity 100.0%; Pred. No. 2.2e-58; Matches 276; Conservative 0; Mismatches 0;
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Please visit our web site (http://genome.gsc.riken.jp/) for further
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                                                                                                                                                                                                                                                                                                                                     /translation="MWQIIFLTEGWDLVLASAYSNERKSVDSTGRRQYQVQNGPCSYTFLDEFTDSCRSSSSYYMSNAVQRDAPLDYDDSVQRLQVLENILENTOWLMKLENYIQDMKKEMVEIQONVVQNQTAVMIEJSTSLLWCDYDDSVQRLQVLENLTDVEAQVLNQTTLELQLLQHCHSISTNKLEKQILDQTSEINKLEJQLLQHKSFLEQKVLDMSGKHSEQLQSMKEQKDELQVLVSKQSSVIDELEKKLVTATVNNSLLQKQQHDLMETVNSLLTMMSSPNSKGSVAIRKEEQTTFRDCAEIFKSGITTSGIYTLTFPNSTEEIKAYCDMDVGGGGWTVIQHREDGSVD
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2459. .2464
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/dev_stage="11 days
274._.1764
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2475
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AGEESNYRIHLTGLTGTAGKISSISQPGSDFSTKDSDNDKCICKCSQMLSGGWWFDAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="GI:12860232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product; ANGIOPOIETIN-2 PRECURSOR (SWISSPROT 035608, evidence: FASTY, 99.6%ID, 100%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="ovary and uterus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/mol_type="mRNA"
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/db_xref="taxon:10090"
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REFERENCE
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Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.niowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciurognathi, Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 792)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: pYX-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is clone was contributed by the Brain Molecular Anatomy Project
/tissue_type="whole eye"
/dev_stage="newborn( 1, 5, 15 days)"
/lab_host="DH108 (T1 phage resistant)"
/clone lib="NIH BMAP HU0"
/clone lib="NIH BMAP HU0"
/clone lib="NIH BMAP HU0"
/site 2: Not I; The library was constructed according
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with Oligo-dT
grimer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:30666956"
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                                   Email: genome res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninol,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira, and Havashiraki,Y., Cokazaki,Y., Muramatsu,M., Inoue,Y., Kira,
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                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nıshi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
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              and Hayashizaki,
RIKEN integrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.5%;
sequence analysis (RISA) system--384-format
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Pred. No. 4.4e
0; Mismatches
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d, adult
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ACCESSION
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Mus musculus
Mus musculus
Eukaryota; Me
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                                                              AA389106.1
AA389106.1
EST.
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                                                                                                                 mp24h01.r1 Life Tech mouse embryo 8 5dpc clone IMAGE:570193 5', mRNA sequence.
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KONNO.H., Fukunishi.Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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e mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RIKEN full-length enriched, adult male kidney"
/note="Site 1: XhoI; Site 2: SstI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAQAGAGAGCGCGCAACTCGAGGTTTTTTTTTTTTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="kidney"
/dev_stage="adult"
/lab_host="SOLR"
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|mol_type="mRNA"
                                                                               GI:2042062
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                                         (house mouse)
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Pred. No. 2.8e-55;
0; Mismatches 5;
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10664019 Mus musculus
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usculus cDNA
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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KEYWORDS
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
AK048622
AK048622.1 GI:26339449
HTC; CAP trapper.
Mus musculus (house mous
                                                                                                                        AK048622

2443 bp mRNA linear HTC 03-.
Mus musculus 16 days embryo head cDNA, RIKEN full-length en
library, clone:Cl30089A05 product:ANGIOPOIETIN-2 PRECURSOR,
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 354)
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Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAGAGAGAATG 1220
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  musculus (house mouse)
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/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site
Sall; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. -8.5dpc embryos. pCMV-SPORT2 vector."
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/dev_stage="8.5dpc embryos"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:570193"
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                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
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                                                                                                                prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                       Encyclopedia Project of Genome Exploration Genomic Sciences Center and Genome Science Division of Experimental Animal Research in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420, 563-573
6 (bases 1 to 2443)
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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/strain="C57BL/6J"
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BB649745
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Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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BB649745 RIKEN full-length enriched, 16
musculus cDNA clone C130089A05 5', mRNA
BB649745
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/ protein_id="BAC33396.1"
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/ db_xxef="gi:26339450"
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/dev_stage="16 days embryo"
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/db_xref="taxon:10090"
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Query Match Best Local S Matches 241

Similarity

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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,X., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A., and Hayashizaki,Y.
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Je Fax: 81-45-503-9216
                 /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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/lab_host="DH10B"
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/sex="mixed"
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/mol_type="mRNA"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
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1 (bases 1 to 912)
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601102294F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3494566 5',
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National Institutes of Health, Mammalian Gene
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Stem cell origin."
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/db_xref="taxon:10090"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome_res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical RESEARCH (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
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Contact: Yoshihide Hayashizaki
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Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T.
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Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
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                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3322402G22"
/tissue_type="head"
/dev_stage="17 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                             organism="Mus musculus"
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2E 1 (bases 1 to 665)

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LOUNDUBLISHED (2001)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tanrumi-kn, Yokohama, Kanagawa, 20,0046, Tanan
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Mus musculus (house mouse)
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Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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e mouse tissues.
CCCTGTGCCTTAGACAGCAGCTGAGAGCTCAGGACGCAAGTTTGCTGAACTCACAGTTTA 1196
                                           GAAAGAGCCTGCTGCGGGACGGAGAAGGCTCTCACTGATGGACTTATTCACACGGCACAG
                                                                        GAAAGAGCCTGCTGCGGGACGAGAAGGCTCTCACTGATGGACTTATTCACACGGGACAGG
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Fax: 81-45-503-9216
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/dev_stage="0 day neonate"
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100.0%; Pr
0;
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Pred. No. 2.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0265 row: M column: 18
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Contact: Robert B.
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                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (Temale) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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350 A-----GTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTGGT
                                                         290 TATCTATTGTTACCAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chardon, P., Iannuccelli, N., Roig, A., Dossat, C., Rogel-Gaillard, C., Roy, A., Schibler, L. and Milan A physical map of the swine genome
                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-NOV-2004) Genoscope - BP 191 91006 EVRY cedex - FRANCE (E-
                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope
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Rogel-Gaillard, C., Bourgeaux, N., Billault, A.,
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suida¢
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Location/Qualifiers
                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="Large White"
/db_xref="taxon:9823"
                                                                                                                                                                                /note="Genoscope sequence ID : IH0AAA34DD10FM1"
                                                                                                                                                                                                                                'sex="male"
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        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                 BX506958 726 bp mRNA
DKFZp779M112_r1 779 (synonym: hncc1) Hon
DKFZp779M112_5', mRNA sequence.
                                                                                                           EST (Poustka,A., Albert,R., Wellenreuther,R., et al.)
Unpublished (2003)
                                                                                             Contact: MIPS
                                                                                                                                                                                Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wel
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G.,
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                       Homo sapiens
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1 (bases 1 to 204)
Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Hirozane, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Carninci, P., Hanagaki, T., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Hodoyama, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Okazaki, Y., Okada, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okado, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, A., Yasunishi, A., Yoshida, K., Yoshiki, A.,
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Best Local Sin Matches 248;
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                                                                                                                                                            204 bp mRNA linear
BB601394 RIKEN full-length enriched, 13 days embr
musculus cDNA clone D430011L06 5', mRNA sequence.
BB601394
Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                   BB601394.1 GI:11509995
EST.
                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone (DKFZp779M112) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       German Genome Project.
No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium
                                                                                                                                                                                                                                                                                                                                                                                           GCAGGGCTGCTCCTTCCTCCAGGACAGC 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATACTGACACTGTAGACTCAGGGGAGAACAAAGAGTCCGTGCAGACCTCTGGAGTGA 1003
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="DKPZp779M112"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="PH108"
/clone_lib="779 (synonym: hncc1)"
/note="Vector: pSport1_Sfi; Site_1: Sf
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0; Mismatches 79;
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182
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   turther details.
                                                                                                                                                                                        Please visit our web site (http://genome.rtc.riken.go.jp) for
                           ACGGCACAGCCCTGTGCCTTAGA 1150
                                                                                                 AGGCACTGGGAAAGAGCCTGCTGCGGGACGAAAGGCTTCACTGATGGACTTATTCAC 112
                                                                                                                                                        ACTGACACTGTAAAATCAGGGGAGAAACAAAGAGTCCGTGCAGAACTCTGGAGTGAGCAG
                                                                                                                                                                                                                                                                    ACTGACACTGTAGACTCAGGGGAGAAACAAAGAGTCCGTGCAGACCTCTGGAGTGAGCAG 1007
                                                                            AGGGACTGGGAAAGAGCCTGCTGCGGGAGGGAGAGGGTCTCACTGATGGACTCATCCAC 181
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="lung"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 13 days embryo
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                                                                                                                                                                                                                                                                                                                                        Score 175.8; DB 2
Pred. No. 2.9e-33;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                           DB 2;
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BU580281
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                                                                                                                                                                                                                                                            Best Local Sig
Matches 172;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ik77g09.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to TR:O35608 O35608 ANGIOPOIETIN 2.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40RP from Gibco
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 p1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endocrine Pancreas Consortium Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 617-495-1812
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                                                                            AGGCTCTCACTGATGGACTTATTCACACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAG 1161
                                                                                                                                                                                     GCCGGGGAGAAGAGAGAGAAGAGACAGGCACTGGGAAAGAGCCCTGCTGCGGGACGGAGA 1101
GCAGAGTACGGGGGAAGAGAGAGACAGGCACTGGGAAAGAGCCTGCTGCGGGACGGAGA
                                              AGGCTCTCACTGATGGACTTATTCACACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAG
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Location/Qualifiers
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"

/strain="129/Sv x CD1"

/db_xref="taxon:10090"

/dev_stage="p.c. 14.5"

/lab_host="E. coli-DH12S (GIBCO)"

/lab_host="E. coli-DH12S (GIBCO)"

/clone_lib="Kaestner ngn3 wt"

/note="Cogan: pancreas; Vector: pSPORT1 (GIBCO); Site_1:

Not I; Site_2: Sal I; The library was prepared by

Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,

2000). The cDNA's were prepared with an oligo containing a

NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/-. The wt library is in
pSPORTI, T7 promoter is 5'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                               13.8%;
96.1%;
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                                                                                                                                                                                                                                                            7; Indels
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Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1303057 seqs, 888780828 residues
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1220
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	.	Score	% Query Match	Length	DB	ID	Description
	Р	47.4	3.9	7218	2	US-08-232-463-14	Sequence 14, Appl
O	N	46.4	3.8	1864	w	-09-468-265-	Sequence 4, Appli
	ω	46.2	3.8	1141	w	US-09-806-708B-22	22
	4.	45.4		20674	w	US-09-641-638-651	65
	ហ	45.4	3.7	20674	w		651,
	თ	44.6		732	ω	US-08-998-416-1036	
	7	44		1141	w	US-09-806-708B-22	22, 1
	80	43.8	3.6	2308	w	US-10-104-047-682	682,
ი	9	42.6		80411	ω	US-09-949-016-15777	15777
_	5		•	93493	w	US-09-949-016-12063	
_	Ε	42.4		. 95020	w	US-09-949-016-13272	1327
	2	42.2		50000	ω	US-09-662-254B-25	
n L	ū	42	,3.4	601	w	US-09-949-016-83375	8337
	14	42	3.4	601	w	US-09-949-016-83376	
_	5	42	3.4	143550	w	US-09-949-016-14143	Sequence 14143, A
G	16	41.8	3.4	832	w	US-09-621-976-2813	2813, A
_	17	41.6	3.4	280	w	US-09-621-976-14588	14588,
_	8	41.6	3.4	32392	w	US-09-662-254B-27	27,
n	9	41.2	3.4	50000	w	US-09-662-254B-24	Sequence 24, Appl
	0	41	3.4	244	w	US-09-621-976-484	484
	21	41	3.4	19124	N	US-08-487-826B-13	
	22	40.6		601	w	US-09-949-016-70227	7022
	23	40.6	ω 	70323	w	US-09-949-016-17594	
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39.8	40	40	40	40	40	40.2	40.2	40.4	40.4	40.4	40.4	40.4	40.4	40.4	40.4	40.4	40.4	40.4	40.4	40.4
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N	w	w	w	ω	ω	N	w	w	w	w	ω	w	w	ω	ω	w	w	w	ω	w
US-08-487-826B-13	US-09-949-016-16113	US-09-331-581-14	US-09-331-581-3	US-09-248-796A-9583	US-08-998-416-191	US-08-611-107-30	US-09-949-016-206713	US-09-949-016-14703	US-09-949-016-14702	US-09-949-016-14701	US-09-949-016-14700	US-09-949-016-14699	US-09-949-016-13926	US-09-949-016-13925	US-09-949-016-13924	US-09-949-016-13923	US-09-949-016-13922	US-09-573-080A-29	US-09-270-767-22773	US-09-270-767-7491
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
13, Appl	16113, A	14, Appl	 Appli 	9583, Ap	191, App	30, Appl	206713,	14703, A	14702, A	14701, A	14700, A	14699, A	13926, A	13925, A	13924, A	13923, A	13922, A	29, Appl	22773, A	7491, Ap

ALIGNMENTS

CURE ATTC REL TELL TIME T	US-08-232- US-08-232- US-08-232- US-08-232- US-08-232- EQUATION OF THE SECURITY OF THE SE
ZIF: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: US/07/935,313 FILING DATE: 26-AUG-1991 ATTORNEY,AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: Linear IMMEDIATE SOURCE: CLONE: pTZ9Dt-F1s	14, Application US/08232463 to. 5570367 to. FORMATION: CANT: DORNER, F. CANT: SCHELFLINGER, F. CANT: SCHELFLINGER, F. CANT: FALKNER, F. G. OF INVENTION: RECOMBINANT FOWLPOX TOF SEQUENCES: 52 ROF SEQUENCES: 52 RESSEE: Foley & Lardner RESSEE: Foley & Lardner RESSEE: 1800 Diagonal Road, Suite 500 TY: Alexandria TE: VA NTRY: USA
n #1.25	VIRUS

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RESULT 2
US-09-468-265-4/c
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/468,265
CURRENT FILING DATE: 1995-12-10
PRIOR APPLICATION NUMBER: 08/484,384
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/284,942
PRIOR FILING DATE: 1994-08-02
PRIOR APPLICATION NUMBER: 07/413,010
PRIOR FILING DATE: 1989-09-25
PRIOR PILING DATE: 1989-09-25
PRIOR PILING DATE: 1989-09-25
PRIOR PILING DATE: 1988-02-26
PRIOR PILING DATE: 1988-02-26
PRIOR PILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 06/882,224
PRIOR APPLICATION NUMBER: 06/882,71,
PRIOR APPLICATION NUMBER: 06/771,374
PRIOR FILING DATE: 1985-08-29
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              Query Match 3.8%; Score 46.4; DB 3; Best Local Similarity 45.4%; Pred. No. 0.005; Matches 167; Conservative 0; Mismatches 201;
                                                                                                     NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1864
TYPE: DNA
ORGANISM: Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-232-463-14
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Patent No. 6379928
GENERAL INFORMATION:
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Best Local S
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berka, Randy M
APPLICANT: Cullen, Daniel
APPLICANT: Gray, Gregory L
APPLICANT: Hayenga, Kirk J
APPLICANT: Lawils, Virgil B
TITLE OF INVENTION: Heterologous Polypeptides Expressed
TITLE OF INVENTION: Making Same and Vectors for Making
FILE REFERENCE: A-42909-5
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les 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.9%; Score 47.4; DB 2;
Llarity 0.8%; Pred. No. 0.0054;
Conservative 221; Mismatches 147;
                                               Length 1864;
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US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
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                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter; LOCATION: (1)..(1141); LOCATION: (1)..(1141); OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters US-09-806-708B-22
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                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                          385
                                                                                                                                                                       265 TTCCTCTCGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATTAATCAGGCC
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VKWRDITCTYVDVWADSWVWWYANWMRCRDVTYTRNNTYCKSYAHSYWYWSNNAMWYRRY 554
                                                                                                                                      TSTNMTNNNNNWWACTNNNNNWWKAYYAHATNNWGCWWNNTDARRTNNTTVMRRRWMT
                                                                                                     AAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTGCT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATAAATTCTAGAGTTTTATTAATTAGAGAAAGGGGATAATAATCTTTTTTAATAATAAT 159
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                                                                                                                                                                                                                                                                               3.8%; Score 46.2; DB 3; ilarity 11.2%; Pred. No. 0.0044; Conservative 230; Mismatches 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/133,200 PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER:
                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  TYPE: DNA
               NAME/KEY: exon
LOCATION: 5552.
                                                 OTHER INFORMATION: exon
                                                               NAME/KEY: exon
LOCATION: 3871..4072
                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: exon
                                                                                                OTHER INFORMATION: exon
                                                                                                                OCATION: 3124..3297
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                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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NAME/KEY: allele LOCATION: 2934 OTHER INFORMATION: 1 NAME/KEY: allele LOCATION: 2947
                                                                                                                                 LOCATION: 2832
OTHER INFORMATION:
                                                                                                                                                            LOCATION: 2623
OTHER INFORMATION: 10-512-318
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                        LOCATION: 1827
OTHER INFORMATION: 10-510-173
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1559
OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION: 10-508-245
NAME/KEY: allele
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OTHER INFORMATION: exon
                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 2341
                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 2323
                                                                                                                                                                                                                                                                                                             LOCATION: 2048
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                      OTHER INFORMATION:
                                                                                                                   NAME/KEY: allele
                                                                                                                                                                                                         NAME/KEY: allele
                                                                                                                                                                                                                       OTHER INFORMATION: 10-512-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 10-508-191 : polymorphic base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 17555..20674
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OTHER INFORMATION: 10-513-365
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NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 1
                     NAME/KEY: allele
LOCATION: 12171
                                                              NAME/KEY: allele
                                                                      LOCATION: 8785
OTHER INFORMATION:
                                                                                              OTHER INFORMATION:
NAME/KEY: allele
                                                                                                                               LOCATION: 8703
OTHER INFORMATION:
NAME/KEY: allele
    OCATION: 12171
OTHER INFORMATION:
                                       OCATION: 8926
OTHER INFORMATION:
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LOCATION: 8608
OTHER INFORMATION: 10-349-47
NAME/KEY:
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OTHER INFORMATION: 10-349-97
                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 8658
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LOCATION: 6611
OTHER INFORMATION: 10-347-348
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OTHER INFORMATION: 10-347-203
NAME/KEY: 4161e
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OTHER INFORMATION: 10-347-165
NAME/KEY: allele
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OTHER INFORMATION: 10-347-74 :
NAME/KEY: allele
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OTHER INFORMATION: 10-346-141
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263
                                                                                                                                                                 NAME/KEY: allele
                                                                                                                                                                                                                                            LOCATION: 7668
OTHER INFORMATION: 10-348-391
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LOCATION: 6534
OTHER INFORMATION: 10-347-271
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OTHER INFORMATION: 10-346-305
NAME/KEY: allele
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OTHER INFORMATION: 10-347-220
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
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OTHER INFORMATION: 10-347-111
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LOCATION: 5903
OTHER INFORMATION:
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LOCATION: 4062
OTHER INFORMATION:
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OTHER INFORMATION:
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PATENT NO. 6794143

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
FILLE GEN-T114XC2D1
CURRENT APPLICATION UNMBER: US/10/170,097
CURRENT APPLICATION NUMBER: US/641,638
APPLICATION NUMBER: US 09/641,638
APRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILLING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/135,267
PRIOR APPLICATION NUMBER: US 60/139,275
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILLING DATE: 1999-02-12
PRIOR FILLING DATE: 1999-02-12

NUMBER OF SEO ID NOS: 1204

PRIOR FILLING DATE: 1999-02-12
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US-10-170-097-651/c
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OTHER INFORMATION: 10-350-332 : polymorphic base C (
NAME/KEY: allele
LOCATION: 13341
OTHER INFORMATION: 10-507-170 : polymorphic base A (
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-321 : polymorphic base A (
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-507-353 : polymorphic base C (
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-507-353 : polymorphic base C (
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 651, Application US/10170097 Patent No. 6794143
NUMBER OF SOFTWARE:
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Best Local Similarity 49.0
Matches 180; Conservative
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SEQ ID NO 651
LENGTH: 206
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NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon
                                                        LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                          NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
                                                                                NAME/KEY: misc feature LOCATION: 17555..20674
                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
FEATURE:
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LOCATION: 5996..6099
OTHER INFORMATION: exon
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LOCATION: 5552..5633
OTHER INFORMATION: exon
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LOCATION: 3871..4072
OTHER INFORMATION: exon
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ORGANISM: Homo sapiens
LOCATION: 1128
DTHER INFORMATION: 10-508-191
                                  NAME/KEY: allele
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LOCATION: 16567.
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THER INFORMATION: exon
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OCATION: 13308..13429
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OTHER INFORMATION: exon 10
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LOCATION: 8645..8854
DTHER INFORMATION: exon
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LOCATION: 7379..7522
DTHER INFORMATION: exon
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LOCATION: 6349..6509
OTHER_INFORMATION: exon
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LOCATION: 5758
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LOCATION: 1123..3123
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OTHER INFORMATION: exon
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FEATURE:
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION:
FEATURE:
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NAME/KEY: allele
LOCATION: 2832
                                  NAME/KEY: allele LOCATION: 5903
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NAME/KEY: allele
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LOCATION: 4088
OTHER INFORMATION:
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LOCATION: 1182
OTHER INFORMATION:
                   LOCATION: 5903
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 4062
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OTHER INFORMATION:
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LOCATION: 3802
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OTHER INFORMATION:
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LOCATION: 2844
OTHER INFORMATION:
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LOCATION: 2341
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LOCATION: 2048
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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LOCATION: 2623
OTHER INFORMATION:
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LOCATION: 2323
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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LOCATION: 2934
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LOCATION: 1570
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US-08-998-416-1036/c
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                                            Sequence 1036, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
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Best Local Similarity
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NAME/KEY: allele
LOCATION: 6338
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LOCATION: 6484
OTHER INFORMATION: 10-347-220
            APPLICANT:
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LOCATION: 6467
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 6183
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OTHER INFORMATION:
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LOCATION: 6375
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    Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
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Pred. No. 0.038;
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Best Local
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COMPUTER: IMP PC DOS/MS DOS
SOFTWARE: PATENTIN PC DOS/MS DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION = 435
PRIOR APPLICATION DATA;
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
DEFENDENCE/NOTETT NUMBER: 38,241
DEFENDENCE/NOTETT NUMBER: 38,241
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INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE
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APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
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Local Similarity 46.3%;
les 146; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.01;
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RESULT 8
US-10-104-047-682/c
US-10-104-047-682/c
; Sequence 682, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
GENERAL INFORMATION: RESEARCH INSTITUTE
; APPLICANT: HELLX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full
; FILE REFERENCE: H1-A0105
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09806708B Patent No. 6784342 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/10/104,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a.,
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ORGANISM: Artificial sequence
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                                                                                                                                                                                                                       CSKWWNNYAAWYTKSSWNYTSRYYRWK 559
                                                                                                                                                                                                                                                                                                                                      TCCTAAAA-----GAACAGAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCA
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                                     6943241el full length cDNA
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Pred. No. 0.02;
27; Mismatches
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; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(80411)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-15777
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; Sequence 15777, Application
; Patent No. 6812339
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1577
LENGTH: 80411
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SEQ ID NO 682
LENGTH: 2308
TYPE: DNA
                                                                                  Query Match
Best Local
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                                                                 Matches
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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17141 AAATGACATCTTTAATTCCTTATCCAAGCTAAAGTACATTTATGTATCATGATATGTTAT 1708:
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                             305 AACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAA 364
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S OF DETECTION
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
LENGTH: 95020
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US-09-949-016-12063
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Best Local (
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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Pred. No. 0.68;
0; Mismatches 81;
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OF DETECTION
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US-09-662-254B-25
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US-09-949-016-13272
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Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6933145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/662,254B
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/086,651
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
NUMBER: OF SEQ ID NOS: 80
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APPLICANT: Li, Yi
APPLICANT: Bawden
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APPLICANT: Bawden, Alison Louise
TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
TITLE OF INVENTION: Vertebrate Cells
FILE REFERENCE: UF-221C1XC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn
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TYPE: DNA
ORGANISM: Amsacta moorei entomopoxvirus
Local
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                                                                                                                                                                                                                                                                                                                                      429
                                    669 CAGACAGACAAGAGCCCCAGCTACTCTCTAGGAAATAATTA
                                                                                                                                                                                                                                                                                                                                                                                                             369
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                                                                                                                                          ATATTATAAATAGAATTTTATATATATGTTCCCTTTTTCGATTGAAATAATAGAATATCTTG 17467
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Pred. No. 0.69;
0; Mismatches 81;
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-83376
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US-09-949-016-83376/c
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; ORGANISM: Human
US-09-949-016-83375
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US-09-949-016-83375/c
                                                                             SOFTWARE: FastSEQ
SEQ ID NO 83376
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Best Local Similarity
Matches 99; Conserv
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83375
                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                     PRIOR FILING DATE: 201
NUMBER OF SEQ ID NOS:
                                                                                                                                                           PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                             ENGTH:
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Query Match

Score 42;

DB 3;

Length 601;

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Search completed: December 12, Job time : 264 secs
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; ORGANISM: Human
US-09-949-016-14143
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SEQ ID NO 14143
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GENERAL INFORMATION:
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Best Local Similarity 51.0%;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING TOWNER: 60/237,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POTYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 143550
                                                                            100975 TAAGAAGTTAGAAA 100988
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                                                                                                               589 TAAAAGAACAGAAA 602
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for Windows Version
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Maximum Match 10
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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8 US-10-789-222-34
8 US-10-789-222-34
9 US-10-317-803-4
15 US-10-317-803-4
15 US-10-44-990-24
17 US-10-433-793-188
18 US-10-433-793-188
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18 US-10-311-455-866
18 US-10-311-455-8114
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19 US-10-257-166-44
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Sequence 102, App	Seguence 313319,	Sequence 11622, A	Sequence 5335, Ap	Sequence 1, Appli	Sequence 240, App	Sequence 1664, Ap	Sequence 10387, A	Sequence 89, Appl	Sequence 1063, Ap	Sequence 1229, Ap	Sequence 305, App	Sequence 386, App	Sequence 1738, Ap	Sequence 64, Appl	Sequence 362, App	Sequence 17606, A	Sequence 130, App	Sequence 93, Appl	Sequence 5922, Ap	Sequence 1091, Ap	Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-10-627-075-1

Sequence 1, Application US/10627075
Publication No. US20040091913A1
GENERAL INFORMATION:
APPLICANT: Livingston et al.
TITLE OF INVENTION: Composition and Method
FILE REFERENCE: 20363-019
CURRENT APPLICATION NUMBER: US/10/627,075
CURRENT FILING DATE: 2003-07-24
CURRENT FILING DATE: 2003-07-24

for Imaging Cells

PRIOR APPLICATION NUMBER: 60/398,583
PRIOR FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 1220

TYPE: DNA ORGANISM: Mus musculus

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                                                                                                                                                                                                                                                                                                                           Matches 1220; Conservative
                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1220; DB 7; Best Local Similarity 100.0%; Pred. No. 2.4e-308;
301 ACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTG
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                                                                                                                                                                                                             TGGACCAGCAGAGCCACAGAGCTTGTTTTAGAAGTCAGTGCAGCCCCCAGCTTTT
                                                                                                                  TGGGACTAATTTAATCAGGAACATGCCACAGAGTGATGAGCCCGAGGAAACCCTGATACA
                                                                                                                                                        ATGGCCAGGGGCTTTTGAACTTAATTAAAAGGGGAAAGTGATTTGCCTGAGCCCACTGAC
                                                                                                  TGGGACTAATTTAATCAGGAACATGCCACAGAGTGATGAGCCCGAGGAAACCCCTGATACA
                                                                                                                                                                                                                                                                                                                           0; Mismatches
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RESULT 2
US-10-764-420-1571
Sequence 1571, Application US/10764420
Publication No. US20050084872A1
GENERAL INFORMATION:
APPLICANT: Lum, Pek Yee
APPLICANT: Lum, Pek Yee
APPLICANT: Dai, Hongyue
TITLE OF INVENTION: Methods For Determination of Invention: Possesses A Define
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Determining Whether
A Defined Biological
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CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR APPLICATION NUMBER: US 60/474,413
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 3683
SOPTWARR: FRSEUSQ for Windows Version 4.0
SEQ ID NO 1571
LENGTH: 2475
TYPE: DNA
ORGANISM: Mus musculus
US-10-764-420-1571
                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09790289; Publication No. US20030165826A1; GENERAL INFORMATION:
; APPLICANT: Caroline Barry
APPLICANT: Ilya Chumakov
; TITLE OF INVENTION: PG-3 and Biallelic Markers Th; FILE REFERENCE: 68 US3. REG
; CURRENT APPLICATION NUMBER: US/09/790,289; CURRENT FILING DATE: 2001-02-23; NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent.pm
; SEQ ID NO 1
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US-09-790-289-1/c
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Best Local
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                                                                                                                                                                                                                                                                                                            LENGTH: 24
NAME/KEY: exon
LOCATION: 26810..26897
OTHER INFORMATION: exon
                                                   NAME/KEY: exon
LOCATION: 10115..10233
OTHER INFORMATION: exo
                                                                                                          OTHER INFORMATION: exon
NAME/KEY: exon
LOCATION: 4627..4718
OTHER INFORMATION: exon
                                                                                                                                                                               FEATURE:

NAME KEY: misc feature
LOCATION: 1..2000
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
NAME/KEY: exon
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Local Similarity 100.0%;
les 276; Conservative (
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LOCATION: 10228

OTHER INFORMATION: 5-392-222 : E
LOCATION: 10286

LOCATION: 10286

LOCATION: 10286

LOCATION: 10370

OTHER INFORMATION: 5-392-280 : E
LOCATION: 39944

LOCATION: 39944

LOCATION: 39944

LOCATION: 39933

OTHER INFORMATION: 4-58-318 : po
NAME/KEY: allele
LOCATION: 3993

OTHER INFORMATION: 4-58-289 : po
NAME/KEY: allele
LOCATION: 41385

OTHER INFORMATION: 4-54-199 : po
NAME/KEY: allele
LOCATION: 41404

OTHER INFORMATION: 4-54-180 : po
NAME/KEY: allele
LOCATION: 4232

OTHER INFORMATION: 4-54-180 : po
NAME/KEY: allele
LOCATION: 69521

OTHER INFORMATION: 99-86-266 : E
NAME/KEY: allele
LOCATION: 69521

OTHER INFORMATION: 99-86-266 : E
NAME/KEY: allele
LOCATION: 69521

OTHER INFORMATION: 4-88-107 : po
NAME/KEY: allele
LOCATION: 72838

OTHER INFORMATION: 5-397-141 : po
NAME/KEY: allele
LOCATION: 59521

OTHER INFORMATION: 5-397-141 : po
NAME/KEY: allele NAME/KEY: exon
LOCATION: 95111.95188
OTHER INFORMATION: exon J
NAME/KEY: exon
LOCATION: 216015..216252
OTHER INFORMATION: exon K NAME/KEY: exon
LOCATION: 237526..238825
OTHER INFORMATION: exon L
NAME/KEY: misc_feature
LOCATION: 238826..240825
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1999
OTHER INFORMATION: 5-390-177 : polymorphic base G or C NAME/KEY: exon LOCATION: 72881..72918 OTHER INFORMATION: exon H NAME/KEY: exon LOCATION: 37377...37466 OTHER INFORMATION: exon NAME/KEY: allele
LOCATION: 4601
OTHER INFORMATION: 5-391-43 : polymorphic base A
NAME/KEY: allele NAME/KEY: exon LOCATION: 75989..76151 OTHER INFORMATION: exon NAME/KEY: exon LOCATION: 50436..50545 OTHER INFORMATION: exon LOCATION: 39704..40858
OTHER INFORMATION: exon T LOCATION: 34261..34404 OTHER INFORMATION: exon NAME/KEY: exon LOCATION: 31357..31471 OTHER INFORMATION: exon NAME/KEY: exon ົດ ч M polymorphic base G or .. polymorphic base A polymorphic base A or G polymorphic base polymorphic base A or C polymorphic base G polymorphic base G polymorphic base insertion of G polymorphic base G or polymorphic base G or Q or C or T or 유 or R a G

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/KEY: allele TION: 123231 R INFORMATION /KEY: allele TION: 123277	KEY: all	R INFORMATION /KEY: allele TION: 122083	LOCATION: 114604 OTHER INFORMATION: NAME/KEY: allele LOCATION: 115716	LOCATION: 011616 OTHER INFORMATION: NAME/KEY: allele	/KEY: allele TION: 108472 R INFORMATION	/KEY: allele TION: 108327 R INFORMATION	/KEY: al	KEY: allele ION: 106407	NAME/KEY: allele LOCATION: 106373 OTHER INFORMATION:	TION: 10439	TION: 10359 R INFORMATI	98963 ORMATI allel	: 9891 FORMAT	ATION: 9802 ER INFORMAT E/KEY: alle	FORMAT	TION: 96190 R INFORMATI /KEY: allel	TION: 9551 R INFORMAT /KEY: alle	Ó	: 9191 FORMAT : alle	LOCATION: 83921 OTHER INFORMATION: NAME/KEY: allele	TION: 8125 R INFORMAT /KEY: alle	Õ
9-12767-143 : polymorphic base C or	99-12767-36 : polymorphic base G or C	-84-334 : polymorphic base A or G	4-86-60 : polymorphic base G or C	4-44-277 : polymorphic base C or T	polymorphic b	-105-86 : polymorphic base A or	-105-08 · polymorphic base to cr	o-19750-196 . Molemouphic hass for	99-12758-102 : polymorphic base A or G	99-12757-318 : polymorphic base C or T	4-87-212 : polymorphic base A or G	99-12755-329 : polymorphic base A or C	99-12755-280 : polymorphic base A or G	5-364-252 : polymorphic base G or T	99-12753-34 : polymorphic base A or T	4-23-326 : polymorphic base A or G	4-21-317 : polymorphic base G or T	4-21-154 : polymorphic base C or T	99-12749-175 : polymorphic base C or T	99-109-358 : polymorphic base A or C	99-12738-248 : polymorphic base A or C	5-398-203 : polymorphic base A or C

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Query Match
Best Local Similarity
Matches 545; Conserv
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NAME/KEY: allele
LOCATION: 123468
OTHER INFORMATION: 9
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LOCATION: 128687
OTHER INFORMATION: 4-35-240 : polymorphic base G
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LOCATION: 128594
OTHER INFORMATION: 4-35-333
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LOCATION: 128333
OTHER INFORMATION: 4-36-261
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LOCATION: 128210
OTHER INFORMATION: 4-36-384
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LOCATION: 126738
OTHER INFORMATION: 4-80-328
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LOCATION: 128330
OTHER INFORMATION: 4-36-264
                             157974 TGGTTGGAGGGCAGTCTGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTAC
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AGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCT
                                                    CTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTAC
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Pred. No. 4.7e-50;
0; Mismatches 265; Indels 38;
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SOFTWARE: Patent.pm
SEQ ID NO 1
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TITLE OF INVENTION: PG-3 and biallelic markers
FILE REFERENCE: 68.WO2
CURRENT APPLICATION NUMBER: US/10/468,582
CURRENT FILING DATE: 2003-08-20
                                                                                                                                                                                                       FEATURE:
NAME/KEY: exon
LOCATION: 34261..34404
OTHER INFORMATION: exon
                          NAME/KEY: exon
LOCATION: 50436..50545
                                                                         LOCATION: 39704..40
OTHER INFORMATION:
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LOCATION: 31357..31471
OTHER INFORMATION: exo
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LOCATION: 37377
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LOCATION: 26810..26
OTHER INFORMATION:
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NAME/KEY: exon
LOCATION: 4627..4718
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LOCATION: 2001..2079
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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NAME/KEY: exon
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LOCATION: 1..2000
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ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: 238826..240825
OTHER INFORMATION: 3'regulatory region
FEATURE:
NAME/KEY: allele
LOCATION: 1999
OTHER INFORMATION: 5-390-177 : polymorph
FEATURE:
NAME/KEY: allele
LOCATIONE: 4601
OTHER INFORMATION: 5-391-43 : polymorph:
                        FEATURE:
NAME/KEY: allele
LOCATION: 69521
OTHER INFORMATION: 4
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LOCATION: 41385
OTHER INFORMATION: 4
FEATURE:
NAME/KEY: allele
LOCATION: 41404
OTHER INFORMATION: 4
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LOCATION: 42232
OTHER INFORMATION: 4
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NAME/KEY: allele
LOCATION: 39973
OTHER INFORMATION: 4
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NAME/KEY: allele
LOCATION: 39944
OTHER INFORMATION: 4
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NAME/KEY: allele
LOCATION: 10370
OTHER INFORMATION: !
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LOCATION: 67475
OTHER INFORMATION:
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NAME/KEY: exon
LOCATION: 95111..95188
OTHER INFORMATION: exon J
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LOCATION: 10228
OTHER INFORMATION:
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LOCATION: 72881..72918
OTHER INFORMATION: exon
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LOCATION: 10286
OTHER INFORMATION:
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LOCATION: 237526..238825
OTHER INFORMATION: exon L
FEATURE:
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NAME/KEY: exon
LOCATION: 216015..216252
COTHER INFORMATION: exon K
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LOCATION: 75989..76151
OTHER INFORMATION: exon I
                       4-88-107 : polymorphic base A or G
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No. 20, 20, 20, 20, 20, 20, 20, 20, 20, 20,				
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orphic base C or Trphic base A or Grphic base C or To base A or G c base A or G	phic base A or G phic base A or C base A or G	hic base A or T	phic base C or T base C or T	c base A or C phic base A or C

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 Sequence 1, Application US/11028971
Publication No. US20050158779A1
GENERAL INFORMATION:
APPLICANT: Caroline Barry
APPLICANT: Ilya Chumakov
TITLE OF INVENTION: PG-3 and Biall
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Best Local Similarity
Matches 545; Conserv
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and Biallelic Markers
 Thereof
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FILE REFERENCE: 68.US3.REG
CURRENT APPLICATION NUMBER: US/11/028,971
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/99/790,289
PRIOR FILING DATE: 2001-02-23
INUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 240825
TYPE: DNA
                                                                                                                                                                                                             FEATURE:
NAME/KEY: exon
75989.
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NAME/KEY: exon
'CATION: 31357..31471
'CATION: exon F
                           FEATURE:
NAME/KEY: exon
LOCATION: 237526..238825
OTHER INFORMATION: exon
                                                                                   LOCATION: 216015..2
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 95111.
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OTHER INFORMATION:
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LOCATION: 72881..72918
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LOCATION: 39704..40858
OTHER INFORMATION: exor
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LOCATION:
VAME/KEY: misc_feature
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LOCATION: 50436..50545
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LOCATION: 26810..26897
OTHER INFORMATION: exo
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..2000
OTHER INFORMATION: 5'regulatory region
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LOCATION: 34261..34404
OTHER INFORMATION: exor
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LOCATION: 4627..4718
THEOREMATION: exon
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LOCATION: 37377..37466
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LOCATION: 10115...10233
OTHER INFORMATION: exon
FEATURE:
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LOCATION: 2001..2079
OTHER INFORMATION: e:
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PEATURE:
NAME/KEY: allele
NAME/TON: 76060
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 39973
OTHER INFORMATION:
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OTHER INFORMATION:
                                           NAME/KEY: allele LOCATION: 91917
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 39944
OTHER INFORMATION:
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LOCATION: 10370
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 81253
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LOCATION: 72838
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LOCATION: 69521
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LOCATION: 41404
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LOCATION: 41385
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION: 3'regulatory
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95349
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Best Local Similarity 64.3
Matches 545; Conservative
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NAME/KEY: allele
LOCATION: 96190
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                             NAME/KEY: allele LOCATION: 108327
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OTHER INFORMATION:
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LOCATION: 106407
OTHER INFORMATION:
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LOCATION: 103593
OTHER INFORMATION:
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LOCATION: 98963
OTHER INFORMATION:
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LOCATION: 98914
OTHER INFORMATION:
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LOCATION: 98024
OTHER INFORMATION:
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LOCATION: 104398
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LOCATION: 97294
OTHER INFORMATION:
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158334
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                                                                                                                                                                            TCACTCAAATATCTATTGTTACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTT
                                                                                                    GAATATCCAAGTGGAGTTTTTTTAAAGA-ATAAAGGTCAGAGCTCAG-AAACTGATGTTT 158395
                                                                                                                                                     AAATTCTAATTTCTCTATTGTAATGTAATGAACTTAATCAGTACAGTGTATTTTTAGAGT
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                       AATGTGCATAACTTAAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCCTTGGAAAA
                                                CTAACGTGACTTAATAACAGATCTTTCTATCCAACTGTTCGGAAATGAAAATCTTTTGTA
                                                                          GTAACTTGATTTAATAA-----
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                                                                                                                                                                                                                                                        Score 238; DB 10;
Pred. No. 4.7e-50;
0; Mismatches 265;
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US-10-317-803-11
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LENGTH: 2424
TYPE: DNA
ORGANISM: M. musculus
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                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                         APPLICANT: Kathleen Myers
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MCDULATION OF ANGIOPOIETIN-2 |
FILE REFERENCE: RTS-0454
CURRENT APPLICATION NUMBER: US/10/317,803
CURRENT FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 244
                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (211)...(1701)
                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 2308
OTHER INFORMATION: n = A,T,C
                                                                  Local Sir
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                                                            h 17.5%; Score 213, DB 7; I Similarity 100.0%; Pred. No. 1.3e-44; 13; Conservative 0; Mismatches 0;
                AAGTGAGC 157727
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Sequence 34, Application US/10789222;
Publication No. US20040186054A1
GENERAL INFORMATION:
APPLICANT: Yu, Qin
TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses
FILE REFERENCE: UPN0003-100 (p3115)
CURRENT APPLICATION NUMBER: US/10/789,222
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US 60/450,582
PRIOR FILING DATE: 2003-02-27
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 2424
TYPE: DNA
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US-10-827-759A-5
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; NAME/KEY: misc_feature
; LOCATION: (2308)..(2308)
; OTHER INFORMATION: n is
US-10-789-222-34
Sequence 5, Application US/10827759A
Publication No. US20040248174A1
GENERRAL INFORMATION:
APPLICANT: The Trustees of the University of Pennsylvania
APPLICANT: Samuel Jotham Reich
APPLICANT: Michael J. Tolentino
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SIRNA
TITLE OF INVENTION: INHIBITION OF ANGIOPOIETIN 1 AND 2 AN
FILE REFERENCE: 43826-0005 US1
CURRENT APPLICATION NUMBER: US/10/827,759A
CURRENT FILING DATE: 2004-04-19
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US-10-789-222-34
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; Pred. No. 1.3e-44;
0; Mismatches 0;
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; PRIOR APPLICATION NUMBER: US 60/463,981
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 5
; LENGTH: 2424
; TYPE: DNA
; ORGANISM: Mus musculus
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US-10-317-803-4
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10317803
Publication No. US20040115640A1
GENERAL INFORMATION:
APPLICANT: Kathleen Myers
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF ANGIOPOIETIN-2 EXPRESSION
FILE REFERENCE: RTS-0454
CURRENT APPLICATION NUMBER: US/10/317,803
CURRENT FILING DATE: 2002-12-11
                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 62705
TYPE: DNA
ORGANISM: H. sapiens
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Best Local Similarity
Matches 335; Conserv
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Best Local Similarity
Matches 213; Conserv
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LOCATION: 2308
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                   GAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTG
                                                           CTTAATTGGGGTGCTTAGGAAATGCCCAGGGTCCTGTAACAGATCGGTTTTTCCCA
                                                                              ---TAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCA
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GCTTAGCACGGCAAAAATCAGTTTCAGACAAAAGAGATCAACTGCTCTCTAGGAAATA
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                                                                                                                                                                                                                                             17.4%;
ilarity 74.3%;
Conservative
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                                                                                                                                                                                                                                            Score 211.8; DB 7;
Pred. No. 1.6e-43;
0; Mismatches 107;
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Pred. No. 1.3e-44;
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GENERAL INFORMATION:
APPLICANT: Olga Bandman
ITILE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 24
LENGTH: 3251
TYPE: DNA
ORGANISM: Homo sapiens
US-10-433-793-187
; Sequence 187, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angio
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/433,793
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Matches 209;
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NAME/KEY: misc feat
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Pred. No. 8.9e-30;
0; Mismatches 69
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Diagnose von mit Angiogenese

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US-10-433-793-188/c
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated
US-10-433-793-187
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 188
LENGTH: 2846
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                            Sequence 188, Application US/10433793
Publication No. US20040142334A1
GENERAL INFORMATION:
                                                                                 Query Match
Best Local
                                                                     Matches
                                                                                                                             OTHER INFORMATION: -10-433-793-188
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Best Local Similarity
Matches 295; Conserv
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NUMBER OF SEQ ID NOS:
SEQ ID NO 187
LENGTH: 2846
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TITLE OF INVENTION: Diagnose von mit Angiogenese
FILE REFERENCE:
               1651
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                                                                                   Similarity
                               CCĄCĄGĄGTGĄTGAGCCCGAGGĄĄĄCCCTGĄTĄCĄGTGĄĄGGĄĄĄĄAGGTGTĄTGTTTGTT
       AAGGAAAGTGATTGATTCGGATACTGACACTGTAGACTCAGGGGAGAACAAAGA
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                                                                  Conservative
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                                                                                                                                      chemically treated genomic DNA
                                                                              11.4%;
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62.1%;
                                                                 Score 139.4; Pred. No. 2.6e
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Pred. No. 1.3e-25;
0; Mismatches 164;
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APPLICANT: OLER, Alexander
APPLICANT: DEBENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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US-10-311-455-866/c
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Publication No. US20030143606A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACAAACGAGCAGACAGACAGAGCCCCAGCTACTCTCTAGGAAA-----TAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAACTITCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCCCTCTAAAAAAACACACGTTTACAAAAACCAAACTTCTTCCTCTTTATTATAATA
                                                                                                                                                                                                                                                                                                                                   TGACACTGTAGACTCAGGGGAGAAACAAAGA 980
                                                                                                                                                                                                                                                                                                                                                               CTAGTGACCCCCTACAGGAAGATAGTGGGTGAGCC-AGGGGGGGGGAGCGGCTGGCTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAACTTTCATTATACTTCAACATTAAAATTATTACCTCAAATATTTTACCAACTTAACA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCT------AAAAGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCCCTTGGAAAAGCACA---TTTACAAGGGCTGATCTTAGCCTTTATATTTTACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TÄÄÄÄATCTTTTÄTÄÄCTTAACTAÄTAATTCÄÄÄÄÄTCÄÄCTÄÄÄÄATCÄÄTÄÄATCTATT
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PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR PELICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2114
LENGTH: 15698
TYPE: DNA
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US-10-311-455-2114/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2114, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                                 Query Match
Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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SEQ ID NO 866
LENGTH: 10710
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

CURRENT FILING DATE: 2002-12-16
                                                                                                                                              OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens
                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: chemically treated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
   7371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 TAAAAAAAAATGTGCATAACTTAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 AATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 TATGTTTGTTTCCTCTCGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATT
ТАРАТТАСАРАРАТАРТАРССАСССАРАТАРАРАРТАТАРАРАДАРТЕРАРТАРАРТАР
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Pred. No. 0.0067;
0; Mismatches 155;
                                                                              Score 54.4; DB Pred. No. 0.012;
                                                              Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 10710;
                                                                                           DB 6;
                                                                                           Length 15698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-45
CURRENT APPLICATION NUMBER: US/10/602,494
CURRENT FILING DATE: 2003-06-23
NUMBER OF SEQ ID NOS: 385
SEQ ID NO 272
LENGTH: 2265
                                                                                                                                                                                                                                                                                          Query Match 4.3%;
Best Local Similarity 52.5%;
Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cathy Lofton-Day
APPLICANT: Andrew Sledziewski
APPLICANT: Jeff Thomas
APPLICANT: Robert W. Day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lori Tonnes-Priddy
APPLICANT: Karen Cardon
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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                                  602
                                                                                                        542 AATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCTAAAAGAACAGAA
                                                                       482 GACTTTACTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTAC
                                                                                                                                                                                                                                                        656 GCCTACAA
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 42
                                                                                                                                                                                                                    ACTITCACTATGCTTTAAAATTAAAGTGATTACCTCAGA
ACTAACACAATACAAATACCCTAAACACACTAAATAAAA
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                                                                                                                                                                                                                                                                                                           Score 52.6; DB 8;
Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                            Length 2265;
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Search completed: December 12, 2005, 15:40:53 Job time : 1003 secs

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